

STIC-Biotech/ChemLib

85648

From: Fredman, Jeffrey  
Sent: Thursday, January 30, 2003 1:46 PM  
To: STIC-Biotech/ChemLib  
Cc: Angell, Jon E  
Subject: FW: RUSH Sequence Database Search Request

RECEIVED

JAN 30 2003

(STIC)

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Angell, Jon E  
Sent: Thursday, January 30, 2003 12:20 PM  
To: Fredman, Jeffrey  
Subject: RUSH Sequence Database Search Request

SEARCH REQUEST FORM  
Scientific and Technical Information Center

Examiner# : 78697  
Art Unit : 1635  
Phone Number: 605-1165  
Date: 1/30/03  
Serial Number: 09/622,846  
MailBox & Bldg/Room Location: CM1-11E12  
Results Format Preferred (circle): Paper

I would like to have a standard search and please include all pending databases performed using the following SEQ. ID NOs. from application : 09/622,846

SEQ ID NO. 16--nucleic acid about 2400 nucleotides long

Thanks,  
Eric

J. Eric Angell  
Art Unit 1635  
CM1 12D15  
703-605-1165  
mailbox CM1 11E12

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
jan.delaval@uspto.gov

Searcher: Jan  
Phone: 4456  
Location: \_\_\_\_\_  
Date Picked Up: 1/30/03  
Date Completed: 1/31/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: W  
Online time: 10

TYPE OF SEARCH: ☒  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: ☒  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 20:58:43 ; Search time 6122 Seconds  
(without alignments)  
11608.796 Million cell updates/sec

Title: US-09-622-846-16

Perfect score: 2442  
Sequence: 1 taccctccagctccgagtc.....ttgttcacgtccctcttg 2442

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pt: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: em\_da: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_ph: \*  
24: em\_pi: \*  
25: em\_pi: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vt: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pin: \*  
35: em\_hcg\_rtd: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hgo\_hum: \*  
40: em\_hgo\_mus: \*  
41: em\_hgo\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2442	100.0	2442	6	AX018772	AX018772 Sequence
2	2440.4	99.9	2442	6	AX018773	AX018773 Sequence
3	2420	99.1	2441	6	AX018774	AX018774 Sequence
4	2420	99.1	4361	9	HUMMH6	J03027 Human MHC C
5	2418.4	99.0	2441	6	AX018775	AX018775 Sequence
6	2399.8	98.3	5589	9	AF523304	AF523304 Homo sapi
7	2399.6	98.3	3640	9	S50740	S50740 HLA-G (7.0E
8	2395.4	98.1	38194	9	AC004193	AC004193 Homo sapi
9	2395.4	98.1	93937	9	AL645929	AL645929 Human DNA
10	2395.4	98.1	148834	9	HS377H14	AL022723 Human DNA
11	2393.8	98.0	5577	9	AF523301	AF523301 Homo sapi
12	2393.8	98.0	5577	9	AF523302	AF523302 Homo sapi
13	2392.2	98.0	5574	9	AF523305	AF523305 Homo sapi
14	2392.2	98.0	5574	9	AF523306	AF523306 Homo sapi
15	2392.2	98.0	5574	9	AF523307	AF523307 Homo sapi
16	2392.2	98.0	5578	9	AF523309	AF523309 Homo sapi
17	2376.6	97.3	5909	9	AF338356	AF338356 Pan trogl
18	2373.4	97.2	81561	9	AF523300	AF523300 Homo sapi
19	2373.4	97.2	81561	9	AB023057	AB023057 Homo sapi
20	2373.4	97.2	105633	9	AL671561	AL671561 Human DNA
21	2373.4	97.1	129818	9	AP000521	AP000521 Homo sapi
22	2371.8	97.1	5588	9	AF523303	AF523303 Homo sapi
23	2370.2	96.7	319486	9	AF055066	AF055066 Homo sapi
24	2361.4	96.7	5587	9	AF523299	AF523299 Homo sapi
25	2353	96.4	5574	9	AF523307	AF523307 Homo sapi
26	2353	96.4	5574	9	AF523308	AF523308 Homo sapi
27	2353	96.4	5574	9	AF523310	AF523310 Homo sapi
28	2353	96.4	5574	9	AF523311	AF523311 Homo sapi
29	2044.4	83.7	37854	9	AC004172	AC004172 Homo sapi
30	1829	74.9	4003	9	HUMMH1A	M80469 Human MHC C
31	1829	74.9	45298	9	AC005404	AC005404 Homo sapi
32	1829	74.9	159178	9	AL669914	AL669914 Human DNA
33	1825.8	74.8	100000	9	AP000519	AP000519 Homo sapi
34	1825.8	74.8	147116	9	AL645935	AL645935 Human DNA
35	1825.8	74.8	162227	9	AB023056	AB023056 Homo sapi
36	1825.8	74.8	162426	2	AC011858	AC011858 Homo sapi
37	1818.4	74.5	122555	2	AL845439	AL845439 Homo sapi
38	1818.4	74.5	159919	2	AL845454	AL845454 Homo sapi
39	1807.4	74.0	4914	2	HUMMH1A	M80468 Human MHC C
40	1802.6	73.8	86441	2	AL390762	AL390762 Homo sapi
41	1784.6	73.1	5668	9	AF338358	AF338358 Pan trogl
42	1780.2	72.9	4745	9	HUMMH1A	M80470 Human MHC C
43	1780.2	72.9	4745	9	HUMMH1A	M96337 Homo sapien
44	1732.4	70.9	6705	9	L47206	L47206 Homo sapien
45	1730.8	70.9	6705	9	L47231	L47231 Homo sapien

#### ALIGNMENTS

RESULT 1  
AX018772  
LOCUS AX018772 2442 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 16 from Patent WO9943851.  
ACCESSION AX018772  
VERSION AX018772.1 GI:10042894  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 2442)  
Mccarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.  
TITLE Hla linked pre-eclampsia and miscarriage susceptibility gene  
JOURNAL Patent: WO 9943851-A 16 02-SEP-1999;

Pred. No. is the number of results predicted by chance to have a

MCCARTHY TOMKIE V (IE); BIRMINGHAM JOHN (IE); JENKINS DAVID M (IE);  
BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE  
KATHLEEN A (IE)

FEATURES  
source location/Qualifiers  
1..2442

/organism="Homo sapiens"

BASE COUNT 485 a 659 c 735 g 563 t

ORIGIN

Query Match 100.0%; Score 2442; DB 6; Length 2442;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGGTCGTGGATCCACCCGAGGCCGCGGAGACCCGCGCAGACCTTC 60  
DB 1 TACTCCGAGTCTCCGGGTCGTGGATCCACCCGAGGCCGCGGAGACCCGCGCAGACCTTC 60  
QY 61 TACCTGGGAGAACCCCAAGGCGGCTTACCAAAATCCCGGGTGGGTCCGGGCGAGGG 120  
DB 61 TACCTGGGAGAACCCCAAGGCGGCTTACCAAAATCCCGGGTGGGTCCGGGCGAGGG 120  
QY 121 CGAGGCTCGTGGGCGGCGTGAACCGAGGGGTCGGGCGCAGTTCTTCACACCCCTCCAGTG 180  
DB 121 CGAGGCTCGTGGGCGGCGTGAACCGAGGGGTCGGGCGCAGTTCTTCACACCCCTCCAGTG 180  
QY 181 GATGATTTGGCTTCGACCTCGGGGTCGCGACGACGCTCTCTCGGGGGTATGACAGATATGC 240  
DB 181 GATGATTTGGCTTCGACCTCGGGGTCGCGACGACGCTCTCTCGGGGGTATGACAGATATGC 240  
QY 241 CTACAGTGGCAGAGATTTACCTCGCCCTGAACGAGACCTCGGCTCTCGGACCCGACGGA 300  
DB 241 CTACAGTGGCAGAGATTTACCTCGCCCTGAACGAGACCTCGGCTCTCGGACCCGACGGA 300  
QY 301 CACTCGGCTCAGATCTTCCAAAGCCGAGTGTAGGCGGCCCAATGTGCTTACCAAGAGAG 360  
DB 301 CACTCGGCTCAGATCTTCCAAAGCCGAGTGTAGGCGGCCCAATGTGCTTACCAAGAGAG 360  
QY 361 ACCTCACTGGAGGCGACGCTGTGAGTGGCTCCACAGATACCTGTGAGAGAGGGAAGA 420  
DB 361 ACCTCACTGGAGGCGACGCTGTGAGTGGCTCCACAGATACCTGTGAGAGAGGGAAGA 420  
QY 421 GATGCTCGAGGCGCGGGTACCAAGGGCAGTGGGGCGCTTCCTGATCTCTGTAGACT 480  
DB 421 GATGCTCGAGGCGCGGGTACCAAGGGCAGTGGGGCGCTTCCTGATCTCTGTAGACT 480  
QY 481 CTGACCTGGCTAGCACAAGAGAGAGAAATGGACCAACTAGAAATTCGCGCT 540  
DB 481 CTGACCTGGCTAGCACAAGAGAGAGAAATGGACCAACTAGAAATTCGCGCT 540  
QY 541 CCCTCTGCTCTGAGGAGAGAAATCTCTGCTGGGTTTCCAGATCTGTACCAAGAGTGA 600  
DB 541 CCCTCTGCTCTGAGGAGAGAAATCTCTGCTGGGTTTCCAGATCTGTACCAAGAGTGA 600  
QY 601 TTCTGAGGCGGCTCTCTCTCTGAGGACATTAAGGATTAAGTCTCTGAGGAGTGA 660  
DB 601 TTCTGAGGCGGCTCTCTCTCTGAGGACATTAAGGATTAAGTCTCTGAGGAGTGA 660  
QY 661 GGGGAGAGACATCTCTGAGAGACTGATGAGGGTTCCTTTGACCCACAGACGCTTG 720  
DB 661 GGGGAGAGACATCTCTGAGAGACTGATGAGGGTTCCTTTGACCCACAGACGCTTG 720  
QY 721 CACCGAGACTTTTCCCGCAGGCGCTGTCTCTGCTCCACACTCAATGTGTGGGGGTC 780  
DB 721 CACCGAGACTTTTCCCGCAGGCGCTGTCTCTGCTCCACACTCAATGTGTGGGGGTC 780  
QY 781 TGACTTCAGGCTCTCTGAGTCCCTTGGCTTCACCTCAGTTCAGAACCGGAGTCCCTGCT 840  
DB 781 TGACTTCAGGCTCTCTGAGTCCCTTGGCTTCACCTCAGTTCAGAACCGGAGTCCCTGCT 840  
QY 841 CCCCCGCTCAGAGACTTAAGACTTTTCCAAAGAAATAGAGATTATCCAGGGTCCGCTTC 900  
DB 841 CCCCCGCTCAGAGACTTAAGACTTTTCCAAAGAAATAGAGATTATCCAGGGTCCGCTTC 900

QY 901 AGCGTGGTCTGAGGCTTCTGTGCTCCCTTCCACCCAGATGATGTTCAATCTTAG 960  
DB 901 AGCGTGGTCTGAGGCTTCTGTGCTCCCTTCCACCCAGATGATGTTCAATCTTAG 960  
QY 961 ATGCTCACATCCAGGCTCTCTGAGTGTCCATGAGAGATGCAAGTCTTGAATTTTC 1020  
DB 961 ATGCTCACATCCAGGCTCTCTGAGTGTCCATGAGAGATGCAAGTCTTGAATTTTC 1020  
QY 1021 TGACTCTTCTTTCAGAGACCCCGCAGAGACACGTACACACACCTCTCTTACATAT 1080  
DB 1021 TGACTCTTCTTTCAGAGACCCCGCAGAGACACGTACACACACCTCTCTTACATAT 1080  
QY 1081 GAGGACACCTTGAAGTCTGAGGCTCTGAGGCTTCTTACCTTCGAGATCATTAATGACTTG 1140  
DB 1081 GAGGACACCTTGAAGTCTGAGGCTCTGAGGCTTCTTACCTTCGAGATCATTAATGACTTG 1140  
QY 1141 CAGGCGGATGGGAGGAGACCAAGACCAAGAGATGAGACTGTGAGACCAAGGCTCAGGG 1200  
DB 1141 CAGGCGGATGGGAGGAGACCAAGACCAAGAGATGAGACTGTGAGACCAAGGCTCAGGG 1200  
QY 1201 GATGAACTTTCAGAGAGTGGGACGCTGTGCTGCTCTTCTGAGAGAGAGAGATATC 1260  
DB 1201 GATGAACTTTCAGAGAGTGGGACGCTGTGCTGCTCTTCTGAGAGAGAGAGATATC 1260  
QY 1261 ACGTCCATGTGACGATGAGAGGCGCTGCGGAGCCCTCATGCTGATGATGATGAGAG 1320  
DB 1261 ACGTCCATGTGACGATGAGAGGCGCTGCGGAGCCCTCATGCTGATGATGATGAGAG 1320  
QY 1321 GGAGATGGAGGACATCATGTGTAGGAGAGAGAGCCCTCTGAGACCTTTAACAG 1380  
DB 1321 GGAGATGGAGGACATCATGTGTAGGAGAGAGAGCCCTCTGAGACCTTTAACAG 1380  
QY 1381 GGTGGTGTGAGGCTGAGGCTGAGAGACCTTACCTTCTCTTCCAGAGCACT 1440  
DB 1381 GGTGGTGTGAGGCTGAGGCTGAGAGACCTTACCTTCTCTTCCAGAGCACT 1440  
QY 1441 CTTCCCTGCGCCACCATCCCATCATGAGGATTCCTTCTGAGGCTGCTTCTGAGCTG 1500  
DB 1441 CTTCCCTGCGCCACCATCCCATCATGAGGATTCCTTCTGAGGCTGCTTCTGAGCTG 1500  
QY 1501 TAGTACCTGAGAGCTGCGGCTGCTGCTGTGAGAGAGAGAGAGAGAGTAAAGAG 1560  
DB 1501 TAGTACCTGAGAGCTGCGGCTGCTGCTGTGAGAGAGAGAGAGAGTAAAGAG 1560  
QY 1561 GGGTACAGAGTGGGCTGAGTTCCTTCTGAGGAGGCTTCTTCAAGCCAGGATAGA 1620  
DB 1561 GGGTACAGAGTGGGCTGAGTTCCTTCTGAGGAGGCTTCTTCAAGCCAGGATAGA 1620  
QY 1621 GTTGGCCCTGCTGCTTACGAGGAGACCATCATCATCATGAGGCTTCAAGCCAGG 1680  
DB 1621 GTTGGCCCTGCTGCTTACGAGGAGACCATCATCATCATGAGGCTTCAAGCCAGG 1680  
QY 1681 CCGTGTGAGCAGACCTTCTTCTTGAAGACCTGTGACATTAAGAGAGATTTAT 1740  
DB 1681 CCGTGTGAGCAGACCTTCTTCTTGAAGACCTGTGACATTAAGAGAGATTTAT 1740  
QY 1741 TACTTGTGATTTAGTATGATGGGACCTGATCCAGTAATTCAGAGTACAGAGAGTTC 1800  
DB 1741 TACTTGTGATTTAGTATGATGGGACCTGATCCAGTAATTCAGAGTACAGAGAGTTC 1800  
QY 1801 CCGGCTAAGAGACACTTATGAGGAGGAGTGGTGGAGAGACCAATCATGCTTCTGCTG 1860  
DB 1801 CCGGCTAAGAGACACTTATGAGGAGGAGTGGTGGAGAGACCAATCATGCTTCTGCTG 1860  
QY 1861 TTTTCTGATCGCCCTGAGGCTGACATGACATTTCTGAGAACTTCGAGGGTCAA 1920  
DB 1861 TTTTCTGATCGCCCTGAGGCTGACATGACATTTCTGAGAACTTCGAGGGTCAA 1920  
QY 1921 GACTAGAGGTTCTCTTGAAGACCTCATAGGCTTCTTCTGAGGCTTCTGAGGAGCA 1980  
DB 1921 GACTAGAGGTTCTCTTGAAGACCTCATAGGCTTCTTCTGAGGCTTCTGAGGAGCA 1980



QY 1981 TTTTCTCCACAGATTGAAAAGAGGAGGAGCTACTCTCAGGCTGCAAGTAAATGAAG 2040  
|||||  
Db 1981 TTTTCTCCACAGATTGAAAAGAGGAGGAGCTACTCTCAGGCTGCAAGTAAATGAAG 2040  
QY 2041 AGGCTGATCCCTGAGATCCCTTGGATCTTGTGTTGGAGCCATGGGGAGCTCACCAC 2100  
|||||  
Db 2041 AGGCTGATCCCTGAGATCCCTTGGATCTTGTGTTGGAGCCATGGGGAGCTCACCAC 2100  
QY 2101 CCCCAATTCCTCTCTGCGCACATCTCTGTGCTCTGACCAAGAGCTGTTTGTTC 2160  
|||||  
Db 2101 CCCCAATTCCTCTCTGCGCACATCTCTGTGCTCTGACCAAGAGCTGTTTGTTC 2160  
QY 2161 TACTCTAGGAGTGAAGTGGCCAGGGCTCTAATGTCTCTCAAGGCTTGTAAATGTA 2220  
Db 2161 TACTCTAGGAGTGAAGTGGCCAGGGCTCTAATGTCTCTCAAGGCTTGTAAATGTA 2220  
QY 2221 CACCCCGGGGGGCTGATGTCTGTGGCTTGTGAGGGGAACAGGGGACATAGCTGTCTA 2280  
|||||  
Db 2221 CACCCCGGGGGGCTGATGTCTGTGGCTTGTGAGGGGAACAGGGGACATAGCTGTCTA 2280  
QY 2281 TGAGTTTCTTTGACTTCAATGTATGTAGCATGTAGGCTGTTTAAAGTGTACCCCT 2340  
|||||  
Db 2281 TGAGTTTCTTTGACTTCAATGTATGTAGCATGTAGGCTGTTTAAAGTGTACCCCT 2340  
QY 2341 CACTGTGACTGATATGAAATTTGTTTCATGAATATTTTCTGTAGTGAACAGCTGCCCT 2400  
|||||  
Db 2341 CACTGTGACTGATATGAAATTTGTTTCATGAATATTTTCTGTAGTGAACAGCTGCCCT 2400  
QY 2401 GTGTGGAGCTGAGTGGCAAGATTGTTTCATGCTTCCCTTTG 2442  
|||||  
Db 2401 GTGTGGAGCTGAGTGGCAAGATTGTTTCATGCTTCCCTTTG 2442

RESULT 2  
AX018773 2442 bp DNA linear PAT 07-SEP-2000  
LOCUS AX018773  
DEFINITION Sequence 17 from Patent WO943851.  
ACCESSION AX018773  
VERSION AX018773.1 GI:10042895  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mccarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,K.A.  
TITLE Hla linked pre-eclampsia and miscarriage susceptibility gene  
JOURNAL Patent: WO 943851 A 17 02-SEP-1999;  
MCCARTHY TOMKIE V (IE); BERMINGHAM JOHN (IE); JENKINS DAVID M (IE);  
BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE  
KATHLEEN A (IE)

FEATURES  
source location/Qualifiers  
1..2442  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 485 a 658 c 735 g 564 t  
ORIGIN

Query Match 99.9%; Score 2440.4; DB 6; Length 2442;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 2441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATCCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGGGAGACCCGCGACACCTC 60  
|||||  
Db 1 TATCCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGGGAGACCCGCGCGACACCTC 60  
QY 61 TACCTGGAGAAACCCCAAGGCGCTTTACCAAAATCCCGCGGTGGGTCCGGGCGAGG 120  
|||||  
Db 61 TACCTGGAGAAACCCCAAGGCGCTTTACCAAAATCCCGCGGTGGGTCCGGGCGAGG 120  
QY 121 CGAGGCTCGGTGGGCGGGGCTGACCGAGAGGGGTGGGCGCAGTCTCAGACCTCCAGTG 180  
|||||  
Db 121 CGAGGCTCGGTGGGCGGGGCTGACCGAGAGGGGTGGGCGCAGTCTCAGACCTCCAGTG 180

QY 181 GATGATTGGCTGAGACTGGGGTCCGACGGAGCCCTCTCCGGGGTATGAACATATGC 240  
|||||  
Db 181 GATGATTGGCTGAGACTGGGGTCCGACGGAGCCCTCTCCGGGGTATGAACATATGC 240  
QY 241 CTACGATGGCAAGATTACCTCGCCCTGACAGAGACCTGCGCTCTCTGACCGCAGCGA 300  
|||||  
Db 241 CTACGATGGCAAGATTACCTCGCCCTGACAGAGACCTGCGCTCTCTGACCGCAGCGA 300  
QY 301 CACTGGGCGTCAGATCTCCAGGCGCAAGTGTAGGGGCGCATGTGGCTGGAACAAAGAG 360  
|||||  
Db 301 CACTGGGCGTCAGATCTCCAGGCGCAAGTGTAGGGGCGCATGTGGCTGGAACAAAGAG 360  
QY 361 AGCCTACCTGAGAGGCGACGTGGGTGAGTGGCTCCACAGATACCTGTGAGAAAGGAGA 420  
|||||  
Db 361 AGCCTACCTGAGAGGCGACGTGGGTGAGTGGCTCCACAGATACCTGTGAGAAAGGAGA 420  
QY 421 GATGCTGCAAGCGCGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTGAGACCT 480  
|||||  
Db 421 GATGCTGCAAGCGCGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTGAGACCT 480  
QY 481 CTCAGGCTGGCCCTAGGCAAGAGAGAGAGAAATGGGACCAACTAGATATGCGCT 540  
|||||  
Db 481 CTCAGGCTGGCCCTAGGCAAGAGAGAGAGAAATGGGACCAACTAGATATGCGCT 540  
QY 541 CCTCTGCTCTGAGGAGAGAGAAATCTCTGGGTTTCCAGATCTCTGTACAGAGATGA 600  
|||||  
Db 541 CCTCTGCTCTGAGGAGAGAGAAATCTCTGGGTTTCCAGATCTCTGTACAGAGATGA 600  
QY 601 TTCTGAGGGCGCGTCTGCTCTCTGAGACATTAAGGATGAAGTCTGAGGGAGTGA 660  
|||||  
Db 601 TTCTGAGGGCGCGTCTGCTCTCTGAGACATTAAGGATGAAGTCTGAGGGAGTGA 660  
QY 661 GGGGAGACAAATCCCGGAAAGATGATCAGGGGTTTCCCTTACCCCAAGAGGCTTGC 720  
|||||  
Db 661 GGGGAGACAAATCCCGGAAAGATGATCAGGGGTTTCCCTTACCCCAAGAGGCTTGC 720  
QY 721 CACGAGACTTTTCCCTCAGGCGCTTGTCTCTGAGCTCACTCAATGTGTGGGGGTC 780  
|||||  
Db 721 CACGAGACTTTTCCCTCAGGCGCTTGTCTCTGAGCTCACTCAATGTGTGGGGGTC 780  
QY 781 TGACTCCAGCTCTCTGAGTCCCTTGGCTCCACTCAGGTGAGAACCGAGGTCCTGCT 840  
|||||  
Db 781 TGACTCCAGCTCTCTGAGTCCCTTGGCTCCACTCAGGTGAGAACCGAGGTCCTGCT 840  
QY 841 CCCCCCTCAGACATGAACTTCCAGAAATGAGAAATTTCCAGGTGCCCGGTTC 900  
|||||  
Db 841 CCCCCCTCAGACATGAACTTCCAGAAATGAGAAATTTCCAGGTGCCCGGTTC 900  
QY 901 AGGCTGCTGCTGGTCTGTGCTCCCTTCCGCCACCGAGTATGTTCAATCTTAGG 960  
|||||  
Db 901 AGGCTGCTGCTGGTCTGTGCTCCCTTCCGCCACCGAGTATGTTCAATCTTAGG 960  
QY 961 ATGCTACATCATCAGGTGCTGCTGAGTGTCCATGAGATGCAAAAGTCTTGAATTTTC 1020  
|||||  
Db 961 ATGCTACATCATCAGGTGCTGCTGAGTGTCCATGAGATGCAAAAGTCTTGAATTTTC 1020  
QY 1021 TGACTCTCTCTCAGACCCGCCCAAGACACAGATGACCCACCCCTTCTTGAATAT 1080  
|||||  
Db 1021 TGACTCTCTCTCAGACCCGCCCAAGACACAGATGACCCACCCCTTCTTGAATAT 1080  
QY 1081 GAGGCAACCTGAGTGTGCTGGGCTCTGAGCTTCTTACCTGCGGAGATCTTACCTGAG 1140  
|||||  
Db 1081 GAGGCAACCTGAGTGTGCTGGGCTCTGAGCTTCTTACCTGCGGAGATCTTACCTGAG 1140  
QY 1141 CAGCGGATGAGGAGAGACAGACCAAGACGTGAGACTCTGTGAGACAGGCGCTGAGG 1200  
|||||  
Db 1141 CAGCGGATGAGGAGAGACAGACCAAGACGTGAGACTCTGTGAGACAGGCGCTGAGG 1200  
QY 1201 GATGGAACCTTCCAGAAAGTGGGAGCTGTGTGCTCTTCTGGAAGAGGAGAGATAC 1260  
|||||  
Db 1201 GATGGAACCTTCCAGAAAGTGGGAGCTGTGTGCTCTTCTGGAAGAGGAGAGATAC 1260

Qy	1261	ACGTCGCATGTGCACGATGAGGGGCTGCGGAGCCCTTCATGCTGAGATGAGTAAGAGG	1320
Db	1261	ACGTCGCATGTGCACGATGAGGGGCTGCGGAGCCCTTCATGCTGAGATGAGTAAGAGG	1320
Qy	1321	GGATATGAGGACATCATGTCTGTAAAGGAAAGCAGAGGCCCTCTGAAAGACCTTTAACG	1380
Db	1321	GGATATGAGGACATCATGTCTGTAAAGGAAAGCAGAGGCCCTCTGAAAGACCTTTAACG	1380
Qy	1381	GGTCGGTGTGAGGGGCTGAGAGACCTTCACCTTCACCTCTCTTCCAGAGCAGT	1440
Db	1381	GGTCGGTGTGAGGGGCTGAGAGACCTTCACCTTCACCTCTCTTCCAGAGCAGT	1440
Qy	1441	CTTTCCTGCCCCACCATCCCATCATGAGATATGCTTGGCTGGCTGTTGTCTCTTCACATG	1500
Db	1441	CTTTCCTGCCCCACCATCCCATCATGAGATATGCTTGGCTGGCTGTTGTCTCTTCACATG	1500
Qy	1501	TATCAGCTGAGAGCTGGGCTGGCTGCTGCTGTGAGAAAGAGAGAGCTCAGATTAAGAG	1560
Db	1501	TATCAGCTGAGAGCTGGGCTGGCTGCTGCTGTGAGAAAGAGAGAGCTCAGATTAAGAG	1560
Qy	1561	GGGTGACAAATGGGGGCTGTGAGTTTTCTTCCCACTGGGGGTTTCAAGCCCCACAGTTGAA	1620
Db	1561	GGGTGACAAATGGGGGCTGTGAGTTTTCTTCCCACTGGGGGTTTCAAGCCCCACAGTTGAA	1620
Qy	1621	GTTGCCCCCTGCTGTTTACTGGGAAGCACCATCCACACTCATGGGCTTACCAGCCTGGG	1680
Db	1621	GTTGCCCCCTGCTGTTTACTGGGAAGCACCATCCACACTCATGGGCTTACCAGCCTGGG	1680
Qy	1681	CCCTGTGTGCGACACCTCTCTCTTTGTAAAGCACTGTACAAATGAGACAGATTAT	1740
Db	1681	CCCTGTGTGCGACACCTCTCTCTTTGTAAAGCACTGTACAAATGAGACAGATTAT	1740
Qy	1741	TACCTTGATGATTTGTAGTATGAGGAGCCTATCCAGTATATCAGAGTTCAGAGAAAGTCTC	1800
Db	1741	TACCTTGATGATTTGTAGTATGAGGAGCCTATCCAGTATATCAGAGTTCAGAGAAAGTCTC	1800
Qy	1801	CTGTGCTAAGGACAGACTTTAGAGGGGCACTGTGTGAGGAGCCACATCTGTTTCCCTTG	1860
Db	1801	CTGTGCTAAGGACAGACTTTAGAGGGGCACTGTGTGAGGAGCCACATCTGTTTCCCTTG	1860
Qy	1861	TTTTTCTGATGCGCCCTGGGCTGCGAGTCAACAATTTCTGGAACCTCTCGAGGGTCCAA	1920
Db	1861	TTTTTCTGATGCGCCCTGGGCTGCGAGTCAACAATTTCTGGAACCTCTCGAGGGTCCAA	1920
Qy	1921	GACTAGAGGATTTCTTAGGACCTCATGAGGCCCTGCGCACCTTTCTGGGCTCTCAGAGACA	1980
Db	1921	GACTAGAGGATTTCTTAGGACCTCATGAGGCCCTGCGCACCTTTCTGGGCTCTCAGAGACA	1980
Qy	1981	TTTTTCTTCCACAGATTGAAAAGAGAGGAGCTACTCTCAGGGCTGCAAGTAAATGTAAGG	2040
Db	1981	TTTTTCTTCCACAGATTGAAAAGAGAGGAGCTACTCTCAGGGCTGCAAGTAAATGTAAGG	2040
Qy	2041	AGGCTATGCTCGAGATGCTTGGGATCTTGTGTGAGGAGCCATGGGGAGAGCTCACCCAC	2100
Db	2041	AGGCTATGCTCGAGATGCTTGGGATCTTGTGTGAGGAGCCATGGGGAGAGCTCACCCAC	2100
Qy	2101	CCCACAATTTCTCTCTGCGCACATCTCTGTGTGCTCTGACCAAGTGTGTTTTGTTC	2160
Db	2101	CCCACAATTTCTCTCTGCGCACATCTCTGTGTGCTCTGACCAAGTGTGTTTTGTTC	2160
Qy	2161	TACTCTAGGCAATGACAGTGCCCAAGGGCTCTAATGTTCTCTCAGGGCTTGTAAATGTGA	2220
Db	2161	TACTCTAGGCAATGACAGTGCCCAAGGGCTCTAATGTTCTCTCAGGGCTTGTAAATGTGA	2220
Qy	2221	CACCCCGGGGGGCTGATGTGTGTGGGTTTGTGAGGGAAACAGGGGACATAGCTGTGCTA	2280
Db	2221	CACCCCGGGGGGCTGATGTGTGTGGGTTTGTGAGGGAAACAGGGGACATAGCTGTGCTA	2280
Qy	2281	TGAGGTTTTCTTGACATCAATATATTTAGACATGTGATGGGCTGTTTAAAGTGTACACCCCT	2340
Db	2281	TGAGGTTTTCTTGACATCAATATATTTAGACATGTGATGGGCTGTTTAAAGTGTACACCCCT	2340
Qy	2341	CACGTGTACATATGAATTTGTTCATGAAATTTTTCTGTAGTGTGAAGACGCTGCCCT	2400

Db 2341 CACGTGACTGATVWGAATTTGTTCAATGATATTTTCTGTAGTGTGAACAGCTGCCCT 2400

0y 2401 GTGTGGACACGATGGCAAGATTTGTTTCATCCCTTCCTTTG 2442

Db 2401 GTGTGGACCTAGTGGCAACATTTGTTTCATGCCCTTCCTTTG 2442

RESULT 3  
AX018774

LOCUS	AX018774	2441 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 18 from Patent WO9943851.				

REVISION	AX018774.1	GI:10042896
VERSION		
ACCESSION	AA018774	
KEYWORDS		

ORGANISM	human.
SOURCE	
REFERENCE	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 2441)  
Mccarthy, T. V., Bermingham, J., Jenkins, D. M., O and Quane, K. A.

and linked pre-eclampsia and miscarriage susceptibility gene  
Patent: WO 9943851-A 18-02-SEP-1999;  
MCCORDEN PLOWMAN V (TR) BRISTOL UNIV (GB)

BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE KATHLEEN A (IE)

FEATURES	Location/Qualifiers
SOURCE	1. .2441

```

400      /organism="Homo sapiens"
401      /db_xref="taxon:9606"
402      CEO = 225
403      EFO =

```

SIZE ORIGIN	400 g	555 g	750 g	555 g
1	100	100	100	100
2	100	100	100	100
3	100	100	100	100
4	100	100	100	100
5	100	100	100	100
6	100	100	100	100
7	100	100	100	100
8	100	100	100	100
9	100	100	100	100
10	100	100	100	100
11	100	100	100	100
12	100	100	100	100
13	100	100	100	100
14	100	100	100	100
15	100	100	100	100
16	100	100	100	100
17	100	100	100	100
18	100	100	100	100
19	100	100	100	100
20	100	100	100	100
21	100	100	100	100
22	100	100	100	100
23	100	100	100	100
24	100	100	100	100
25	100	100	100	100
26	100	100	100	100
27	100	100	100	100
28	100	100	100	100
29	100	100	100	100
30	100	100	100	100
31	100	100	100	100
32	100	100	100	100
33	100	100	100	100
34	100	100	100	100
35	100	100	100	100
36	100	100	100	100
37	100	100	100	100
38	100	100	100	100
39	100	100	100	100
40	100	100	100	100
41	100	100	100	100
42	100	100	100	100
43	100	100	100	100
44	100	100	100	100
45	100	100	100	100
46	100	100	100	100
47	100	100	100	100
48	100	100	100	100
49	100	100	100	100
50	100	100	100	100
51	100	100	100	100
52	100	100	100	100
53	100	100	100	100
54	100	100	100	100
55	100	100	100	100
56	100	100	100	100
57	100	100	100	100
58	100	100	100	100
59	100	100	100	100
60	100	100	100	100
61	100	100	100	100
62	100	100	100	100
63	100	100	100	100
64	100	100	100	100
65	100	100	100	100
66	100	100	100	100
67	100	100	100	100
68	100	100	100	100
69	100	100	100	100
70	100	100	100	100
71	100	100	100	100
72	100	100	100	100
73	100	100	100	100
74	100	100	100	100
75	100	100	100	100
76	100	100	100	100
77	100	100	100	100
78	100	100	100	100
79	100	100	100	100

Query Match	99.1%;	Score 2420;	DB 6;	Length 2441;
Best Local Similarity	100.0%;	Pred. No. 0;		

Matches 2420;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------------	--------------	----	------------	----	--------	----	------	----

27 1 TATCCCGGAGCTCCTGGGACGCCGAGGAGGCGGAGACCCGCACAGACCCTC 60  
db 1 TATCCCGGAGCTCCTGGGACGCCGAGGAGGCGGAGACCCGCACAGACCCTC 60

61 TACCTGGAGAACCCCAAGGCGCTTATCCAAAATCCCCGGGTGGAGCGGCGAGG 120

Db 61 TACTGGGAGAACCCCAAGGCGCTTTACCAAAATCCCCGGGGTGGCTCCGGCGAGGG 120

QY 121 CGAGGCTGGTGGGCGGCGCTGACCGAGGGGGTGGGGCCAGCTTCTCACACCCCTCCAGTG 180

Db 121 CGAGCGCTGGGTGGGCGGGGCTGACCGAGGGGGTGGGGCCAGGTTCTCACACCCCTCCAGTG 180

QY 181 GATGATTGGCTGGACCTGGGGTCCGACGAGCCCTCCTCCGGGGTATGACAGTATGC 240

Dd 181 GATGATTGGCTGGCACCCTGGGGTCCGACGGAGCCCTCTCCCGGGTATGAACAGTATGC 240

241 CTAACGATGCGCAAGCAATTAACCTCGCCCTGAAAGAGGAGACTGCGCTTCCTGACCCGAGCGGA 300

[illegible]

Db 301 CACTGGGCTCAGATCTCCAGGCGAAGTGTGAGGGGCCAATGTGGCTGAACAAAGGAG 360

OY 361 AGCCTACCTGGAGGCAACGTGCCTGGAGTGGCTCCACAGATTAAGGCGAAGA 420

Db 361 AGCCTACCTGAGGGCACCTGGCGTGGAGTGGCTCCACAGATACCTGGAGAACGGGAAGCA 420

QY 421 GATGCTGAGCGCGGGGTACCAAGGGGCAATGGGGCCCTCCTGATCTCTTAGACCT 480

Dd 421 GATGCTGCAGCCGCGGGTACCAAGGGCACTGGGGCGCCCTCCCTGATCTCCTGTAGACCT 480

[illegible]

101 CAGGCGCCGGGAGGAAATGGACCACTAGATAATCGCCCT 349

Oy 541 CCTGTGCTCCGAGAGAGAGAAATCTCTGGGTTTCCAGATCCTGTACAGAGAGTGA 600  
 |||||  
 Db 541 CCTGTGCTCCGAGAGAGAGAAATCTCTGGGTTTCCAGATCCTGTACAGAGAGTGA 600  
 Oy 601 TTCTGAGGCCCCCTCTCTCTCTGAGCAATTAAAGGATGAAGTCTGTGAGGAGTGA 660  
 |||||  
 Db 601 TTCTGAGGCCCCCTCTCTCTCTGAGCAATTAAAGGATGAAGTCTGTGAGGAGTGA 660  
 Oy 661 GGGGAAGCAATCCTGTGAGAGATGATCAGGGGTTCCCTTTGACCCCAACAGAGCTTGG 720  
 |||||  
 Db 661 GGGGAAGCAATCCTGTGAGAGATGATCAGGGGTTCCCTTTGACCCCAACAGAGCTTGG 720  
 Oy 721 CACAGAGACTTTCCCTCAGAGCTTTGTTCTCTGCTCACACTCAATGTGTGGGGTTC 780  
 |||||  
 Db 721 CACAGAGACTTTCCCTCAGAGCTTTGTTCTCTGCTCACACTCAATGTGTGGGGTTC 780  
 Oy 781 TGACTCCAGCTCTCTGTGAGTCCCTTGCCCTCCACTCAGGTGAGAACCGGAGGCTTCTCT 840  
 |||||  
 Db 781 TGACTCCAGCTCTCTGTGAGTCCCTTGCCCTCCACTCAGGTGAGAACCGGAGGCTTCTCT 840  
 Oy 841 CCCCCGCTCAGAGACTAGAACTTTCCAGGAATAGGAGATTATCCAGGTGGCGGTTC 900  
 |||||  
 Db 841 CCCCCGCTCAGAGACTAGAACTTTCCAGGAATAGGAGATTATCCAGGTGGCGGTTC 900  
 Oy 901 AGGCTGTGTCTGGGTTCTGTCTCTCCCTCCACCCAGAGTATCTGTTCAATCTTAGG 960  
 |||||  
 Db 901 AGGCTGTGTCTGGGTTCTGTCTCTCCCTCCACCCAGAGTATCTGTTCAATCTTAGG 960  
 Oy 961 ATGGTTCACATCCAGTGTCTGTGAGTGTCCATGAGAGATGCAAAAGTCTTGAATTTTC 1020  
 |||||  
 Db 961 ATGGTTCACATCCAGTGTCTGTGAGTGTCCATGAGAGATGCAAAAGTCTTGAATTTTC 1020  
 Oy 1021 TGACTCTTCTCTCAGACCCCCCAAGACACAGGTGACCCACACCTCTCTTACTAT 1080  
 |||||  
 Db 1021 TGACTCTTCTCTCAGACCCCCCAAGACACAGGTGACCCACACCTCTCTTACTAT 1080  
 Oy 1081 GAGGCCACCTCAGAGTGTCTGGGCTTCTTACCTCTGCGAGATCATACTGACTGG 1140  
 |||||  
 Db 1081 GAGGCCACCTCAGAGTGTCTGGGCTTCTTACCTCTGCGAGATCATACTGACTGG 1140  
 Oy 1141 CAGCGGATGGGAGAGACCAAGACAGTGTGAGTGTGTGAGAACCAAGGCTCAGGG 1200  
 |||||  
 Db 1141 CAGCGGATGGGAGAGACCAAGACAGTGTGAGTGTGTGAGAACCAAGGCTCAGGG 1200  
 Oy 1201 GATGAACCTTCCAGAAAGTGTGAGTGTGTCTCTTGTGAGAGAGAGAGATAC 1260  
 |||||  
 Db 1201 GATGAACCTTCCAGAAAGTGTGAGTGTGTCTCTTGTGAGAGAGAGAGATAC 1260  
 Oy 1261 AGGTGCATGTGAGCATGAGGGGCTGCCGAGACCCCTCATGTGATGAGTAAGAG 1320  
 |||||  
 Db 1261 AGGTGCATGTGAGCATGAGGGGCTGCCGAGACCCCTCATGTGATGAGTAAGAG 1320  
 Oy 1321 GAGGATGGAGGATCATGTCTGTGTAGGAAAGAGAGGCTCTGTGAAGACCTTTAAGAG 1380  
 |||||  
 Db 1321 GAGGATGGAGGATCATGTCTGTGTAGGAAAGAGAGGCTCTGTGAAGACCTTTAAGAG 1380  
 Oy 1381 GGTGCGTGTGAGAGGCTGGGGGTCAAGAGACCTTCACTTACCTTCCAGAGACAT 1440  
 |||||  
 Db 1381 GGTGCGTGTGAGAGGCTGGGGGTCAAGAGACCTTCACTTACCTTCCAGAGACAT 1440  
 Oy 1441 CTTCCCTGCCACATCCCATCATGAGGTATGCTTCTGCTGCTGTTGCTTGAAGCTG 1500  
 |||||  
 Db 1441 CTTCCCTGCCACATCCCATCATGAGGTATGCTTCTGCTGCTGTTGCTTGAAGCTG 1500  
 Oy 1501 TACTCATGGAGCTGGGCTGCTGTGTGTGTGAGAAAGAGAGCTCAGGTAAAGAG 1560  
 |||||  
 Db 1501 TACTCATGGAGCTGGGCTGCTGTGTGTGTGAGAAAGAGAGCTCAGGTAAAGAG 1560  
 Oy 1561 GGGTGAACAATGGGCTGTGATTTCTGTCCACTGGGGGTTTCAAGCCCAAGGTAGAA 1620  
 |||||  
 Db 1561 GGGTGAACAATGGGCTGTGATTTCTGTCCACTGGGGGTTTCAAGCCCAAGGTAGAA 1620  
 Oy 1621 GTGTGCCCTGTGTTACTGTGGAGACCATTCACATCATGAGGCTTACCCAGCTGGG 1680

Db 1621 GTGTGCCCTGTGTTACTGGGAAGACCATTCACATCATGAGGCTTACCCAGCTGGG 1680  
 |||||  
 Oy 1681 CCCGTGTGCCAGACCTTCTCTTTTGTAAAGACCTGTGACATATGAGAGACATTTAT 1740  
 |||||  
 Db 1681 CCCGTGTGTGCAGACCTTCTCTTTTGTAAAGACCTGTGACATATGAGAGACATTTAT 1740  
 Oy 1741 TACCTGTATGATTGTAGTATGGGAGACCTGATCCAGTAATTCACAGTCCAGAAAGTTC 1800  
 |||||  
 Db 1741 TACCTGTATGATTGTAGTATGGGAGACCTGATCCAGTAATTCACAGTCCAGAAAGTTC 1800  
 Oy 1801 CTTGGCTTAAGAGACACCTTTAGAGAGGCACTTGTGTGAGGACCCACATCTCTTCTTG 1860  
 |||||  
 Db 1801 CTTGGCTTAAGAGACACCTTTAGAGAGGCACTTGTGTGAGGACCCACATCTCTTCTTG 1860  
 Oy 1861 TTTTCTCTGATGCGCCCTGGGCTGTGCACATATTTCTGGAACCTTCTGAGGCTCAA 1920  
 |||||  
 Db 1861 TTTTCTCTGATGCGCCCTGGGCTGTGCACATATTTCTGGAACCTTCTGAGGCTCAA 1920  
 Oy 1921 GACTAGAGGTTCCCTTAGAGACCTCATGCGCCCTGCCACTTCTGCGCTCTCAGAGACA 1980  
 |||||  
 Db 1921 GACTAGAGGTTCCCTTAGAGACCTCATGCGCCCTGCCACTTCTGCGCTCTCAGAGACA 1980  
 Oy 1981 TTTTCTCTCCACAGATTTGAAAAGAGGAGAGCTACTCTCAGGCTGCAAGTATGAAAG 2040  
 |||||  
 Db 1981 TTTTCTCTCCACAGATTTGAAAAGAGGAGAGCTACTCTCAGGCTGCAAGTATGAAAG 2040  
 Oy 2041 AGGCTGATCCCTGAGATCCCTTGAGATCTTGTGTGGAGCAATGGGAGAGCTCACCCAC 2100  
 |||||  
 Db 2041 AGGCTGATCCCTGAGATCCCTTGAGATCTTGTGTGGAGCAATGGGAGAGCTCACCCAC 2100  
 Oy 2101 CCCCAATTTCCCTCTGTGGCCACATCTCTGTGTCTGTGACAGAGTGTGTTTGTTC 2160  
 |||||  
 Db 2101 CCCCAATTTCCCTCTGTGGCCACATCTCTGTGTCTGTGACAGAGTGTGTTTGTTC 2160  
 Oy 2161 TACTGTAGGACGTAGACAGTGTCCAGAGGCTCTAATGTGTCTCTCAGGCTGTAAATGTA 2220  
 |||||  
 Db 2161 TACTGTAGGACGTAGACAGTGTCCAGAGGCTCTAATGTGTCTCTCAGGCTGTAAATGTA 2220  
 Oy 2221 CACCCGGGGGGGCGATGTGTGTGGGTTGTGAGGGGAACAGGAGACATAGCTGTGCTA 2280  
 |||||  
 Db 2221 CACCCGGGGGGGCGATGTGTGTGGGTTGTGAGGGGAACAGGAGACATAGCTGTGCTA 2280  
 Oy 2281 TGAGTCTCTTTGACTTCATATGATATGAGCATGTGATGAGGCTGTTTAAAGTGTACCCCT 2340  
 |||||  
 Db 2281 TGAGTCTCTTTGACTTCATATGATATGAGCATGTGATGAGGCTGTTTAAAGTGTACCCCT 2340  
 Oy 2341 CACTGTGACTGATATGATTTGTTCATGATATTTCTGTAGTGTGAACAGCTGCCCT 2400  
 |||||  
 Db 2341 CACTGTGACTGATATGATTTGTTCATGATATTTCTGTAGTGTGAACAGCTGCCCT 2400  
 Oy 2401 GTGTGGAGCTAGTGGCAAG 2420  
 |||||  
 Db 2401 GTGTGGAGCTAGTGGCAAG 2420

RESULT 4  
 HUMH6  
 LOCUS 4361 bp DNA linear PRI 02-MAY-1996  
 DEFINITION Human MHC class I HLA-6.09 gene, complete cds.  
 ACCESSION J03027  
 VERSION J03027.1 GI:187602  
 KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene; major histocompatibility complex.  
 SOURCE Homo sapiens (clone: HLA6.0.) DNA.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 4361)  
 Geraghty, D.E., Koller, B.H. and Orr, R.T.  
 A human major histocompatibility complex class I gene that encodes a protein with a shortened cytoplasmic segment  
 Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9145-9149 (1987)

MIDLINE	88097444
PUBMED	3480354
COMMENT	Draft entry and computer-readable sequence for [1] kindly provided by H.T.Orr, 22-SEP-1987.
FEATURES	location/Qualifiers
source	1..4361
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="HLA6.0."
	/cell_line="721.144"
	/cell_type="lymphoblast"
gene	680..4038
	/gene="MHC HLA-6.09"
exon	680..855
	/gene="MHC HLA-6.09"
	/note="putative"
	/number=1
prim_transcript	<783..>4038
	/gene="MHC HLA-6.09"
	/note="MHC HLA 6.0 mRNA and introns"
CDS	join(783..855,985..1254,1481..1756,2356..2631,2754..2870,3314)..3318)
	/gene="MHC HLA-6.09"
	/codon_start=1
	/protein_id="AA08745.1"
	/db_xref="GI:386874"
	/translation="MYMAPRTLLFLLSGALVLTETWAGSHSMRYESAASVRGGEPRFTAMGYVDTPQVFRRSDSCAPRMEPRAPRWEOGPEYEEETRNTKAHAQTDRMLQTRRGIVNDSSEASSHTLWMICDLSGSDRLRGYEYAYDGKDYLATINEDIRSWTAA DPAAGISKRRCCEAANYAEQRARAYLEGTGVEMLRHYLENKEMLORADPPKTVTHNPV FYEATILSRCKMALGFYPAEIILTWORDEDOTDVLEVETRPAGDSTPDKMAAVVPSSG EERRYCHVQHGGELPEPLTLRWKQSSLPTIPIMGIVAGLVLAAYVTGAAYAAVMRK KSSD"
sig_peptide	783..854
	/gene="MHC HLA-6.09"
mat_peptide	join(855,985..1254,1481..1756,2356..2631,2754..2870,3314)..3315)
	/gene="MHC HLA-6.09"
	/product="unnamed"
	856..984
intron	/gene="MHC HLA-6.09"
	/number=1
exon	985..1254
	/gene="MHC HLA-6.09"
	/number=2
intron	1255..1480
	/gene="MHC HLA-6.09"
	/number=2
exon	1481..1756
	/gene="MHC HLA-6.09"
	/number=3
intron	1757..2355
	/gene="MHC HLA-6.09"
	/number=3
exon	2356..2631
	/gene="MHC HLA-6.09"
	/number=4
intron	2632..2753
	/gene="MHC HLA-6.09"
	/number=4
exon	2754..2870
	/gene="MHC HLA-6.09"
	/number=5
intron	2871..3313
	/gene="MHC HLA-6.09"
	/number=5
exon	3314..3346
	/gene="MHC HLA-6.09"
	/number=6
intron	3347..3487
	/gene="MHC HLA-6.09"
	/number=6
exon	3488..3535

		/gene="MHC HLA-6.09"
intron		/number=7 3536.3702
		/gene="MHC HLA-6.09"
exon		/number=7 3703.24038
		/gene="MHC HLA-6.09"
		/number=8 4033.4038
		/gene="MHC HLA-6.09"
BASE COUNT	915 a 1191 c 1264 g 991 t	
ORIGIN	Chromosome 6p21.3; 323 bp upstream of XbaI site.	
Query Match	99.1%; Score 2420; DB 9; Length 4361;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 2420; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TATCCCGAATCTCCGGTGTGGGATCCACCCCGAGGCGCGGGAGACCCCGACAGACCTC	60
Db	1320 TATCCCGAATCTCCGGTGTGGGATCCACCCCGAGGCGCGGGAGACCCCGACAGACCTC	1379
QY	61 TACCTGGGAGAACCCCAAGGCGCCTTTACCAAAATCCCGCGGGTGGTCTCGGCGAGAG	120
Db	1380 TACCTGGGAGAACCCCAAGGCGCCTTTACCAAAATCCCGCGGGTGGTCTCGGCGAGAG	1439
QY	121 CGAGGCTCGGTGGGCGGGGCTGACCGAGGGGGTGGGCCAGGTTCTACACCTCCAGTG	180
Db	1440 CGAGGCTCGGTGGGCGGGGCTGACCGAGGGGGTGGGCCAGGTTCTACACCTCCAGTG	1499
QY	181 GATGATTGGCTGGACCTGGGGTCCGACGAGACGCTCTCCGCGGGTATGACAGTATGC	240
Db	1500 GATGATTGGCTGGACCTGGGGTCCGACGAGACGCTCTCCGCGGGTATGACAGTATGC	1559
QY	241 CTACGATGGCAAGGATTACCTCGCCTGACAGAGACCTCGCTCCTGACCGACGCGA	300
Db	1560 CTACGATGGCAAGGATTACCTCGCCTGACAGAGACCTCGCTCCTGACCGACGCGA	1619
QY	301 CACTCGGGCTCAAGATCCCAAGCGCAAGTGTAGGCGGCAATGTGGTGTGAACAAGAG	360
Db	1620 CACTCGGGCTCAAGATCCCAAGCGCAAGTGTAGGCGGCAATGTGGTGTGAACAAGAG	1679
QY	361 AGCCTACCTGAGGGACAGTGGTGGAGTGGCTCCACAGATACCTGAGAGAACGGAGAA	420
Db	1680 AGCCTACCTGAGGGACAGTGGTGGAGTGGCTCCACAGATACCTGAGAGAACGGAGAA	1739
QY	421 GATGCTGCAAGCGCGGGGATACAGGGGCAAGTGGGGCCCTCCTGTATCTCTGTAGACT	480
Db	1740 GATGCTGCAAGCGCGGGGATACAGGGGCAAGTGGGGCCCTCCTGTATCTCTGTAGACT	1799
QY	481 CTCAGCTTGCCCTACACACAAGAGAGAGAAATGGGACCAACACTGTGATATGGCCCT	540
Db	1800 CTCAGCTTGCCCTACACACAAGAGAGAGAAATGGGACCAACACTGTGATATGGCCCT	1859
QY	541 CCCTCTGGTCTGAGGGAAGAGATCTCTGGGTTTCCAGATCCTGTACCAAGAGATGA	600
Db	1860 CCCTCTGGTCTGAGGGAAGAGATCTCTGGGTTTCCAGATCCTGTACCAAGAGATGA	1919
QY	601 TTCAGAGGCGCCCTGCTCTCTCTGGGACCAATTAAAGGATTAAGTCTGTGAGGAGTGA	660
Db	1920 TTCAGAGGCGCCCTGCTCTCTCTGGGACCAATTAAAGGATTAAGTCTGTGAGGAGTGA	1979
QY	661 GGGGAGAGCAATCCCTGGAAGACTGATAGAGGGTTCCCTTGGACCCCAACAGACCTTGG	720
Db	1980 GGGGAGAGCAATCCCTGGAAGACTGATAGAGGGTTCCCTTGGACCCCAACAGACCTTGG	2039
QY	721 CACCAAGACTTTTCCCTCAGGCTTGTCTCTGCTCACACTCAATGTGTGGGGTC	780
Db	2040 CACCAAGACTTTTCCCTCAGGCTTGTCTCTGCTCACACTCAATGTGTGGGGTC	2099
QY	781 TGACTCCAGCTCTCTGTAGTCCCTTGGCTCCACTCAGAGTGTAGAACGGAGGTCCCTGCT	840
Db	2100 TGACTCCAGCTCTCTGTAGTCCCTTGGCTCCACTCAGAGTGTAGAACGGAGGTCCCTGCT	2159

QY	841	CCCCCGCTAGAGACTAGAACTTTCCAAAGAAATAGAGATTATCCAGGTGCCGTGTCC	900
Db	2160	CCCCCGCTAGAGACTAGAACTTTCCAAAGAAATAGAGATTATCCAGGTGCCGTGTCC	2219
QY	901	AGGCTGTGTCTGGGTTCTGTCTCCCTTCCCAACCCAGGTATCTGGTTCACTTTAGG	960
Db	2220	AGGCTGTGTCTGGGTTCTGTCTCCCTTCCCAACCCAGGTATCTGGTTCACTTTAGG	2279
QY	961	ATGGTTCACATCCAGAGGTCTGTGAGGTGCCATGAGAGATGCAAAAGTGTGAATTTTC	1020
Db	2280	ATGGTTCACATCCAGAGGTCTGTGAGGTGCCATGAGAGATGCAAAAGTGTGAATTTTC	2339
QY	1021	TGACTCTTCTTTACAGACCCCCCCAAGACACAGGTGACCACCAACCTGTCTTGACTAT	1080
Db	2340	TGACTCTTCTTTACAGACCCCCCCAAGACACAGGTGACCACCAACCTGTCTTGACTAT	2399
QY	1081	GAGGCCACCTGAGGTGTCTGGGCTTGGGGCTTCATCCCTGGGGATCATATGACCTGG	1140
Db	2400	GAGGCCACCTGAGGTGTCTGGGCTTGGGGCTTCATCCCTGGGGATCATATGACCTGG	2459
QY	1141	CAGGGGATGGGGAGGAGACAGACCCAGAGACGTGGAGCTGTGGAGACAGGCGTCAGG	1200
Db	2460	CAGGGGATGGGGAGGAGACAGACCCAGAGACGTGGAGCTGTGGAGACAGGCGTCAGG	2519
QY	1201	GATGGAACCTTCAGAAGTGGGAGCAGTGTGTGGTGTCTTGAGAGAGACAGAGATAC	1260
Db	2520	GATGGAACCTTCAGAAGTGGGAGCAGTGTGTGGTGTCTTGAGAGAGACAGAGATAC	2579
QY	1261	ACGTGCCATGTGCAGCATGAGGGGGCTGGCCGAGGCCCTCATGTCTAATGAGATGAAG	1320
Db	2580	ACGTGCCATGTGCAGCATGAGGGGGCTGGCCGAGGCCCTCATGTCTAATGAGATGAAG	2639
QY	1321	GGAGATGGAGGCATCATGTCTGTATAGAGAAAGAGAGAGCCTTCGAAGACTTTAACAG	1380
Db	2640	GGAGATGGAGGCATCATGTCTGTATAGAGAAAGAGAGAGCCTTCGAAGACTTTAACAG	2699
QY	1381	GGTGTGTGTGAGGGGCTGGGGGATCAGAGACCCCTCACCTTCACCTTCCCAAGAGAGT	1440
Db	2700	GGTGTGTGTGAGGGGCTGGGGGATCAGAGACCCCTCACCTTCACCTTCCCAAGAGAGT	2759
QY	1441	CTTCCCTGCCACCATATCCCATATATGGGTATGTGTCTGGCTTGGTTGTCTTGACATG	1500
Db	2760	CTTCCCTGCCACCATATCCCATATATGGGTATGTGTCTGGCTTGGTTGTCTTGACATG	2819
QY	1501	TAGTACTAGAGAGTGGCGTGCATGTGTGTGTGAGAAAGAAAGAGCTCAGGTAAAGAG	1560
Db	2820	TAGTACTAGAGAGTGGCGTGCATGTGTGTGTGAGAAAGAAAGAGCTCAGGTAAAGAG	2879
QY	1561	GGGTACACAAGTGGGGGTCTGAATTTTCTTGTCTGCACATGGGGGTTTCAGAGCCCAAGTAGAA	1620
Db	2880	GGGTACACAAGTGGGGGTCTGAATTTTCTTGTCTGCACATGGGGGTTTCAGAGCCCAAGTAGAA	2939
QY	1621	GTGTCCCTGCCCTGTACTGTAGGAGACACATACACATCATATGGGCTTACCAGCTGTGG	1680
Db	2940	GTGTCCCTGCCCTGTACTGTAGGAGACACATACACATCATATGGGCTTACCAGCTGTGG	2999
QY	1681	CCCTGTGGCCAGACACCTCTCTTTTGTAAAGACCTGTGACAAATGAAGAGACATTTAT	1740
Db	3000	CCCTGTGGCCAGACACCTCTCTTTTGTAAAGACCTGTGACAAATGAAGAGACATTTAT	3059
QY	1741	TACCTTGAATGATTGATGATGAGGGACCTATCCAGTATCACAGGTACAGAGAAAGTTC	1800
Db	3060	TACCTTGAATGATTGATGATGAGGGACCTATCCAGTATCACAGGTACAGAGAAAGTTC	3119
QY	1801	CCTGCCTAAGGACAGACCTTAAGAGGGCAATGGTGCAGAGACCCACATCTGCTTCTTGG	1860
Db	3120	CCTGCCTAAGGACAGACCTTAAGAGGGCAATGGTGCAGAGACCCACATCTGCTTCTTGG	3179
QY	1861	TTTTTTCAGTACGCCCTGGGCTGTCACTACACATTTTGTGAGAAATCTTCAGAGGCTCAA	1920
Db	3180	TTTTTTCAGTACGCCCTGGGCTGTCACTACACATTTTGTGAGAAATCTTCAGAGGCTCAA	3239
QY	1921	GACTAGAGAGTTCTCTTAGGACCTCATATGGCCCTGCACCTTTCTGGCCTCTCAGAGACA	1980

Db	3240	GACTAGGAGGTTCCCTTAGGACCTCATATGACCCTGGCACCTTCTTGCCCTTCACAGGACA	3299
Qy	1981	TTTTTCTCCACAGATTAAAAAGGAGGAGCTACTCTCAGGCTGCACAGTATGAAG	2040
Db	3300	TTTTTCTCCACAGATTAAAAAGGAGGAGGCTACTCTCAGGCTGCACAGTATGAAG	3359
Qy	2041	AGGCTGATCCCTGAGATCCCTGGGATCTTGTTGGTAGCCATGGGGAGCTCACCCAC	2100
Db	3360	AGGCTGATCCCTGAGATCCCTGGGATCTTGTTGGTAGCCATGGGGAGCTCACCCAC	3419
Qy	2101	CCCAATAATTCCTCCTGTGGCCACATCTCTGTGGTCTGACACAGTCTGTGTTTGTTC	2160
Db	3420	CCCAATAATTCCTCCTGTGGCCACATCTCTGTGGTCTGACACAGTCTGTGTTTGTTC	3479
Qy	2161	TACTTAGCAGTACAGTGCACGGGCTCTATGTGTCTCAGGCTTGTAAATGTGA	2220
Db	3480	TACTTAGCAGTACAGTGCACGGGCTCTATGTGTCTCAGGCTTGTAAATGTGA	3539
Qy	2221	CACCCCGGGGGGCGATGTGTGGTGTGTGAAGGGGAACAGGGGCATACTCTGTGA	2280
Db	3540	CACCCCGGGGGGCGATGTGTGGTGTGTGAAGGGGAACAGGGGCATACTCTGTGA	3599
Qy	2281	TGAGGTTCTTGGACTTCATGATATTTGACATGTATGTGGGCTGTTTAAAGTGCACCCCT	2340
Db	3600	TGAGGTTCTTGGACTTCATGATATTTGACATGTATGTGGGCTGTTTAAAGTGCACCCCT	3659
Qy	2341	CACGTGACTGATATGAATTTGTTCAATGAAATTTTTCTGTAGTGAAGACGTGCCT	2400
Db	3660	CACGTGACTGATATGAATTTGTTCAATGAAATTTTTCTGTAGTGAAGACGTGCCT	3719
Qy	2401	GTGTGGAGCTGAGTGGCAAG	2420
Db	3720	GTGTGGAGCTGAGTGGCAAG	3739

LOCUS	AX018775	2441 bp	DNA	1 linear	PAT 07-SEP-2006
DEFINITION	Sequence 19 from Patent WO9943851.				
ACCESSION	AX018775				
KEYWORDS	AX018775.1 GI:10042897				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Mccarthy,T.V., Bermingham,J., Jenkins,D.M., O and Quane,R.A.				
AUTHORS	1 (bases 1 to 2441)				
TITLE	Hla linked pre-eclampsia and miscarriage susceptibility gene				
JOURNAL	Patent: WO 9943851-A 19 02-SEP-1999;				
	MCCARTHY TOMMIE V (IE); BERRINSHAM JOHN (IE); JENKINS DAVID M (IE);				
	BRIEN MARGARET O (IE); NAT UNIVERSITY OF IRELAND CORK (IE); QUANE				
	KATHLEEN A (IE)				
FEATURES	Location/Qualifiers				
source	1..2441				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	488 a	658 c	735 g	560 t	
ORIGIN					
Query Match	99.0%;	Score 2418.4;	DB 6;	Length 2441;	
Best Local Similarity	100.0%;	Pred. No. 0;	1;	Indels	0
Matches 2419;	Conservative	0;	Mismatches		
1	TACTCCCGAGTCTCTCGGGGTGTGGGATCCACCCGAGGCGCGGGAGACCCGCCGACGACCTTC	60			
1	TACTCCCGAGTCTCTCGGGGTGTGGGATCCACCCGAGGCGCGGGAGACCCGCCGACGACCTTC	60			
61	TACCTGGAGACACCCCAAGGCGCCTTTACCAAAATCCCGCGGGGTGGGTCTCGGGCGAGGG	120			
61	TACTTGGAGACACCCCAAGGCGCCTTTACCAAAATCCCGCGGGGTGGGTCTCGGGCGAGGG	120			

QY 121 CGAGGCTCGGTGGGCGGGGCTGACCCGAGGGGCTGGGCCAGGTTCTTCACACCTCCAGT 180  
 Db 121 CGAGGCTCGGTGGGCGGGGCTGACCCGAGGGGCTGGGCCAGGTTCTTCACACCTCCAGT 180  
 QY 181 GATGATTTGGTCCGACCCGCGGGGCTCGACGAGCCCTCTCCCGGGGATATAGACATATG 240  
 Db 181 GATGATTTGGTCCGACCCGCGGGGCTCGACGAGCCCTCTCCCGGGGATATAGATATG 240  
 QY 241 CTACGATGCAAGGATTAACCTCGCCCTGAACGAGACCTGCGCTCTCCGACCCGACCGA 300  
 Db 241 CTACGATGCAAGGATTAACCTCGCCCTGAACGAGACCTGCGCTCTCCGACCCGACCGA 300  
 QY 301 CACGCGGCTCGATCTCCAAAGGCGGAGTGGAGGCGGCGCAATGGCTGCAAAAGAGG 360  
 Db 301 CACGCGGCTCGATCTCCAAAGGCGGAGTGGAGGCGGCGCAATGGCTGCAAAAGAGG 360  
 QY 361 AGCCCTACGAGGAGGACGTCGTCGAGTGGCTCCACAGATACCTGGAGAAAGGAGGA 420  
 Db 361 AGCCCTACGAGGAGGACGTCGTCGAGTGGCTCCACAGATACCTGGAGAAAGGAGGA 420  
 QY 421 GATGCTGAGGCGCGGGGTACGAGGGGAGTGGGGGCGCTCCGATCTCTCTAGACCT 480  
 Db 421 GATGCTGAGGCGCGGGGTACGAGGGGAGTGGGGGCGCTCCGATCTCTCTAGACCT 480  
 QY 481 CTCAGCCTGGCTAGCACAAAGAGAGGAGAAATGGAGCAACACAGATATCGCCCT 540  
 Db 481 CTCAGCCTGGCTAGCACAAAGAGAGGAGAAATGGAGCAACACAGATATCGCCCT 540  
 QY 541 CCCCTGTGCTGAGGAGGAGGAGGATCCCTCGGGTTTCAGATCTGTTACCAAGATGA 600  
 Db 541 CCCCTGTGCTGAGGAGGAGGAGGATCCCTCGGGTTTCAGATCTGTTACCAAGATGA 600  
 QY 601 TTCTGAGGGGCGGCTGCTGCTCTGAGGACAAATTAAGGATGAAGTCTGAGGAGATGA 660  
 Db 601 TTCTGAGGGGCGGCTGCTGCTCTGAGGACAAATTAAGGATGAAGTCTGAGGAGATGA 660  
 QY 661 GGGGAAAGCAATCCCTGGAAGAGTGAATGAGGGTCCCTTTGACCCCAAGAGCCCTGG 720  
 Db 661 GGGGAAAGCAATCCCTGGAAGAGTGAATGAGGGTCCCTTTGACCCCAAGAGCCCTGG 720  
 QY 721 CACGAGACCTTTCCCGCTGAGGCTGTTGCTGCTGCTCACACTCAATGTTGAGGGGTC 780  
 Db 721 CACGAGACCTTTCCCGCTGAGGCTGTTGCTGCTGCTCACACTCAATGTTGAGGGGTC 780  
 QY 781 TGACTCAGCTCTCTGAGTCCCTTGGGCTCTCACTCAGTCAAGACCGAGGTCCTGCT 840  
 Db 781 TGACTCAGCTCTCTGAGTCCCTTGGGCTCTCACTCAGTCAAGACCGAGGTCCTGCT 840  
 QY 841 CCCCCGCTCAGAGACTGAACCTTCCAAAGGATAGAGATTAATCCAGGGTCCGCTGCT 900  
 Db 841 CCCCCGCTCAGAGACTGAACCTTCCAAAGGATAGAGATTAATCCAGGGTCCGCTGCT 900  
 QY 901 AGGCTGTGTGCTGCTGCTGCTCTCCCTCCAGGATATGCTTCATTTAG 960  
 Db 901 AGGCTGTGTGCTGCTGCTGCTCTCCCTCCAGGATATGCTTCATTTAG 960  
 QY 961 ATGGTCATCTCAGAGTGTGCTGAGTGTCCCATGAGAGATGAATGCTTAATTTTC 1020  
 Db 961 ATGGTCATCTCAGAGTGTGCTGAGTGTCCCATGAGAGATGAATGCTTAATTTTC 1020  
 QY 1021 TGACTCTTCTTGAAGACCCGCCAAGACACAGCTGACCAACCTGCTTTGACTAT 1080  
 Db 1021 TGACTCTTCTTGAAGACCCGCCAAGACACAGCTGACCAACCTGCTTTGACTAT 1080  
 QY 1081 GAGGCTACCTGAGTGTGCTGGGCGCTTACCTTCGAGATCATATGACCTGG 1140  
 Db 1081 GAGGCTACCTGAGTGTGCTGGGCGCTTACCTTCGAGATCATATGACCTGG 1140  
 QY 1141 CAGCGGATGGGAGAGACAGACAGAGAGTGAAGTCTGAGAGACAGGCTTGACGG 1200  
 Db 1141 CAGCGGATGGGAGAGACAGACAGAGAGTGAAGTCTGAGAGACAGGCTTGACGG 1200  
 QY 1201 GATGAAACCTTCCAGAAAGTGGGAGCTGTGTGTGCTCTTCTGAGAGAGAGATAC 1260  
 Db 1201 GATGAAACCTTCCAGAAAGTGGGAGCTGTGTGTGCTCTTCTGAGAGAGAGATAC 1260  
 QY 1261 ACGTGCCATGTGACATGAGAGGCTCCGAGACCCCTCATGTGATGAGTAAAGAG 1320  
 Db 1261 ACGTGCCATGTGACATGAGAGGCTCCGAGACCCCTCATGTGATGAGTAAAGAG 1320  
 QY 1321 GAGATGAGGCTCATGTGCTTGAAGGAAAGAGAGGCTCTCTGAAAGCTTTAAG 1380  
 Db 1321 GAGATGAGGCTCATGTGCTTGAAGGAAAGAGAGGCTCTCTGAAAGCTTTAAG 1380  
 QY 1381 GGTGCGGTGAGGCGTGGGGGTCAGAGACCTCACCTTACCTCTCCAGACAT 1440  
 Db 1381 GGTGCGGTGAGGCGTGGGGGTCAGAGACCTCACCTTACCTCTCCAGACAT 1440  
 QY 1441 CTTCCTGCGCCACCATCCCATCATGAGGATGCTGTGCTGCTGCTGCTGCTG 1500  
 Db 1441 CTTCCTGCGCCACCATCCCATCATGAGGATGCTGTGCTGCTGCTGCTGCTG 1500  
 QY 1501 TAGTCACGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 Db 1501 TAGTCACGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 QY 1561 GGTGACAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 Db 1561 GGTGACAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 QY 1621 GGTGACAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 Db 1621 GGTGACAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 1681 CCTGTGTGCGGACGCTCTCTTTTGAAGACCTGTGACATGAAGAGATTTAT 1740  
 Db 1681 CCTGTGTGCGGACGCTCTCTTTTGAAGACCTGTGACATGAAGAGATTTAT 1740  
 QY 1741 TACCTGATGATTTAGTATGAGGACCTGATCCAGTAATTCAGAGTGAAGAGTTC 1800  
 Db 1741 TACCTGATGATTTAGTATGAGGACCTGATCCAGTAATTCAGAGTGAAGAGTTC 1800  
 QY 1801 CCGGCTAAGGACAGACCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 Db 1801 CCGGCTAAGGACAGACCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
 QY 1861 TTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
 Db 1861 TTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920  
 QY 1921 GACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980  
 Db 1921 GACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980  
 QY 1981 TTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040  
 Db 1981 TTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040  
 QY 2041 AGGCTGATCCCTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100  
 Db 2041 AGGCTGATCCCTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100  
 QY 2101 CCGACATCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160  
 Db 2101 CCGACATCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160  
 QY 2161 TACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220  
 Db 2161 TACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220  
 QY 2221 CACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280  
 Db 2221 CACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280  
 QY 2281 TGAGGTTCTTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2340  
 Db 2281 TGAGGTTCTTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2340



Db	1800	TACCTGGGAACCCCAAGGCGCTTTTACCAAAATCCCTGGGGGTGTGTCGGGCGAGGG	1859
QY	121	CGAGGCTCGGTGGGGGGGGGTGACGAGGGGGGTGGGGCCAGGTTCTACACCTCCAGTG	180
Db	1860	CGAGGCTCGGTGGGGGGGGGTGACGAGGGGGGTGGGGCCAGGTTCTACACCTCCAGTG	1919
QY	181	GATGATTGAGCTGGGACCTGGGGTCCGACGGAGCGCTCTCCGGGGATGTAACAGTATGC	240
Db	1920	GATGATTGAGCTGGGACCTGGGGTCCGACGGAGCGCTCTCCGGGGATGTAACAGTATGC	1979
QY	241	CTACGATGCAAGGATTTACTGGCCCTGAACAGAGACCTGGGCTCTGTGACCCGACGGGA	300
Db	1980	CTACGATGCAAGGATTTACTGGCCCTGAACAGAGACCTGGGCTCTGTGACCCGACGGGA	2039
QY	301	CACGCGGCGTCAGATCCTCCCAAGGCAAGGTGAGGGGGCCCAATGGCTGTAACAAAGAG	360
Db	2040	CACGCGGCTCAGATCTCTCAAGGCAAGGTGAGGGGGCCCAATGGCTGTAACAAAGAG	2099
QY	361	AGCCTACCTGGAGGACACGTGCTGGAGTGGCTCCACAGATACCTGGAAGACGGGAAGA	420
Db	2100	AGCCTACCTGGAGGACACGTGCGTGGAGTGGCTCCACAGATACCTGGAAGACGGGAAGA	2159
QY	421	GATGCTCCAGCGCGCGGGTACAGGGGGCAGTGGGGGCGCTCCCTGATCTCTGTAGACT	480
Db	2160	GATGCTCCAGCGCGCGGGTACAGGGGGCAGTGGGGGCGCTCCCTGATCTCTGTAGACT	2219
QY	481	CTCAGCCTGGGCTCAGACACAGGAGAGAGAAATGGGACCAACCTGTGAATATCGGCT	540
Db	2220	CTCAGCCTGGGCTCAGACACAGGAGAGAGAAATGGGACCAACCTGTGAATATCGGCT	2279
QY	541	CCCTCTGCTCTGAGGAGAGAGANTCCTCTGGGTTTCCAGATCCTGTACACAGAGATGA	600
Db	2280	CCCTCTGCTCTGAGGAGAGAGANTCCTCTGGGTTTCCAGATCCTGTACACAGAGATGA	2339
QY	601	TTCTGAGGGCCCGTCTGCTCTGTGGACAAATTAGGATGAAGTCTTGAGGAGATGGA	660
Db	2340	TTCTGAGGGCCCGTCTGCTCTGTGGACAAATTAGGATGAAGTCTTGAGGAGATGGA	2399
QY	661	GGGGAAGCAATCCCTGGAAGACTGTATCAGGGGTTCCCTTACCCACAGACGCTTGG	720
Db	2400	GGGGAAGCAATCCCTGGAAGACTGTATCAGGGGTTCCCTTACCCACAGACGCTTGG	2459
QY	721	CACCAGGACTTTTCCCTCAGGCGCTTGTCTGTGCTCACACTCAATGTGTGGGGGTC	780
Db	2460	CACCAGGACTTTTCCCTCAGGCGCTTGTGTCTGTGCTCACACTCAATGTGTGGAGGTC	2519
QY	781	TGACTCAGCTCTCTGAGTCCCTTGGCCCTCCACTAGSTCAGAACGGAGTCCCTGCT	840
Db	2520	TGACTCAGCTCTCTGAGTCCCTTGGCCCTCCACTAGSTCAGAACGGAGTCCCTGCT	2579
QY	841	CCCCGCGTCAGAGCTGTAGACTTTGCCAAGGAATAGAGATTATCCAGAGTCCCGTGCC	900
Db	2580	CCCCGCGTCAGAGCTGTAGAACTTTGCCAAGGAATAGAGATTATCCAGAGTCCCGTGCC	2639
QY	901	AGGCTGGTGTGGGTCTGTGCTCCCTTCCACCACCGAGATCTGGTTCATTTCTTAGG	960
Db	2640	AGGCTGGTGTGGGTCTGTGCTCCCTTCCACCACCGAGATCTGGTTCATTTCTTAGG	2699
QY	961	ATGGTCACATCAGGTGCTCTGTGAGTGTCCATGAGAGATSCAAATGTCTTGAATTTTC	1020
Db	2700	ATGGTCACATCAGGTGCTCTGTGAGTGTCCATGAGAGATSCAAAGTGTCTTGAATTTTC	2759
QY	1021	TGACGCTTCCTTTAGAGCCCCCAAGACACAGTAGACACACCTGTCTTTGACAT	1080
Db	2760	TGACGCTTCCTTTAGAGCCCCCAAGACACAGTAGACACACCTGTCTTTGACAT	2819
QY	1081	GAGGCAACCTTGAGGTCTGTGGGCTCTTGAGGTTTCTACCTGCGAGATCATACTGACCTGG	1140
Db	2820	GAGGCAACCTTGAGGTCTGTGGGCTCTTGAGGTTTCTACCTGCGAGATCATACTGACCTGG	2879
QY	1141	CAGCGGATGGGAGACCAAGACCAAGACGTGTGAGCTGTGTGAGACCAAGGCTTGACGG	1200

```
Db 2880 CAGGGGATGGGGAGGACCAACCCAGACGTGCAGCTCTGGAGACCAAGCCCTGCAGAG 2939
OY 1201 GATGGAACCTTTCAGAACTGGGACAGCTGTGTGTGCTTGTGAGAGAGAGAGATAC 1260
Db 2940 GATGGAACCTTTCAGAACTGGGACAGCTGTGTGTGCTTGTGAGAGAGAGAGATAC 2999
OY 1261 ACCTGACATGTGACAGATGAGAGGGCTGCCGAGCCCTCATGTGTGAGATGGAATGAGAG 1320
Db 3000 ACCTGACATGTGACAGATGAGAGGGCTGCCGAGCCCTCATGTGTGAGATGGAATGAGAG 3059
OY 1321 GGAGATGGAGGACATCATGTGTGTAGGGAAGCAAGAGCCCTCTGTGAGAGACCTTTAAG 1380
Db 3060 GGAGATGGAGGACATCATGTGTGTAGGGAAGCAAGAGCCCTCTGTGAGAGACCTTTAAG 3119
OY 1381 GGTGCGGTGTGAGGGGTGGGGGTGAGAGACCCCTCAGCTTCCCTTCCAGAGCAGT 1440
Db 3120 GGTGCGGTGTGAGGGGTGGGGGTGAGAGACCCCTCAGCTTCCCTTCCAGAGCAGT 3179
OY 1441 CTTCCTGCCCCACCATCCCATCATGTGGGTATCGTTGCTGGGCTGTGTCTTGCAGCTG 1500
Db 3180 CTTCCTGCCCCACCATCCCATCATGTGGGTATCGTTGCTGGGCTGTGTCTTGCAGCTG 3239
OY 1501 TAGTCACGTGAGCTCGGCTGCTCTGTGCTGTGAGAGAAAGAGAGCTCAGGTAAAGAG 1560
Db 3240 TAGTCACGTGAGCTCGGCTGCTCTGTGCTGTGAGAGAAAGAGAGCTCAGGTAAAGAG 3299
OY 1561 GGGTACAGAGTGGGGGTCTGAGTTTCTTGTCCACAGTGGGGTTTCAAGCCCAAGTAGAA 1620
Db 3300 GGGTACAGAGTGGGGGTCTGAGTTTCTTGTCCACAGTGGGGTTTCAAGCCCAAGTAGAA 3359
OY 1621 GTGCGCCCTGCTGTGACGTGAGGAGACCATCCACACTATGAGGCTTACCAGCTGGG 1680
Db 3360 GTGCGCCCTGCTGTGACGTGAGGAGACCATCCACACTATGAGGCTTACCAGCTGGG 3419
OY 1681 CCGTGTGTGACAGACCTTCTTTTGTAAAGACCTGTGACAAATGAAAGACAGATTAT 1740
Db 3420 CCGTGTGTGACAGACCTTCTTTTGTAAAGACCTGTGACAAATGAAAGACAGATTAT 3479
OY 1741 TACTGTGATTTGTGTGTGTGTGAGGAGCTGATCCCAATATCAGAGTACAGAGAGGTC 1800
Db 3480 TACTGTGATTTGTGTGTGTGTGAGGAGCTGATCCCAATATCAGAGTACAGAGAGGTC 3539
OY 1801 CCGGCTAAAGAGACCTTAAAGAGGAGGAGTGTGAGAGACCCACATCTGCTTCTTG 1860
Db 3540 CCGGCTAAAGAGACCTTAAAGAGGAGGAGTGTGAGAGACCCACATCTGCTTCTTG 3599
OY 1861 TTTTCTCTGAT - CGCCCTGGGTCTGAGTACACATTTTGTGAAACTTCTCAGAGGTC 1918
Db 3600 TTTTCTCTGATCCCGCCCTGGGTCTGAGTACACATTTTGTGAAACTTCTCAGAGGTC 3659
OY 1919 AAGACTAGAGAGTCTCTTGTGAGACCTATGTGGCCCTGACACTTCTGTGGCCTTCACAGA 1978
Db 3660 AAGACTAGAGAGTCTCTTGTGAGACCTATGTGGCCCTGACACTTCTGTGGCCTTCACAGA 3719
OY 1979 CATTTCCTTCCACAGATTGAAAAGAGGAGGAGTACTCTCAGGCTCAGATAGTATGAA 2038
Db 3720 CATTTCCTTCCACAGATTGAAAAGAGGAGGAGTACTCTCAGGCTCAGATAGTATGAA 3779
OY 2039 GGAGGCTGATCCCTGAGATCTTTGGGATCTTGTGTGGAG - CCAATGGGGAGCTACAC 2097
Db 3780 GGAGGCTGATCCCTGAGATCTTTGGGATCTTGTGTGGAGCCCAATGGGGAGCTACAC 3839
OY 2098 CACCCCAACAATTCCTCTGTGGCACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2157
Db 3840 CACCCCAACAATTCCTCTGTGGCACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3899
OY 2158 TTCTACTTGAAGCAGTACAGTGCAGGAGGCTCTATGTGTGTGTGTGTGTGTGTGTGTGTGT 2217
Db 3900 TTCTACTTGAAGCAGTACAGTGCAGGAGGCTCTATGTGTGTGTGTGTGTGTGTGTGTGTGT 3959
OY 2218 TGACACCCCGGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2277
Db 3960 TGACACCCCGGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4019
```

```
OY 2278 CTATGAGGTTTCTTGTGACTGTAATGTATGTGAGCATGTATGGGCTGTTTAAAGTGCACC 2337
Db 4020 CTATGAGGTTTCTTGTGACTGTAATGTATGTGAGCATGTATGGGCTGTTTAAAGTGCACC 4079
OY 2338 CCTCAGTGTGATGATATGAAATTTGTTTCATGAAATTTTTCGTGTGATGGAAGAGCTGC 2397
Db 4080 CCTCAGTGTGATGATATGAAATTTGTTTCATGAAATTTTTCGTGTGATGGAAGAGCTGC 4139
OY 2398 CCTGTGTGGGACTGAGTGGCAAGATTTTGTATGCTTCCCTTTG 2442
Db 4140 CCTGTGTGGGACTGAGTGGCAAGATTTGTTTCATGCTTCCCTTTG 4184

RESULT 7
LOCUS S50740 3640 bp DNA linear PRI 08-MAY-1993
DEFINITION HLA-G (7.0E)-putative non-polymorphic antigen [human, Genomic, 3640
ACCESSION S50740
VERSION S50740.1 GI:259087
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3640)
AUTHORS Tamaki, J.
TITLE Analysis of polymorphism at the human class I MHC locus, HLA-G
JOURNAL Hokkaido Igaku Zasshi 67 (5), 583-594 (1992)
MEDLINE 93051989
PUBMED 1427601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gtbls9.120998] from the original journal article.
this sequence comes from Fig. 5.
FEATURES
source 1..3640
location/Qualifiers
1..3640
/gene="Homo sapiens"
/db_xref="taxon:9606"
1..3640
/gene="HLA-G"
/note="putative non-polymorphic antigen"
/allele="7.0E"
BASE COUNT 725 a 1021 c 1091 g 803 t
ORIGIN
Query Match 98.3%; Score 2399.6; DB 9; Length 3640;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2423; Conservative 0; Mismatches 19; Indels 2; Gaps 1;
OY 1 TACTCCGAGTCCCGGGTGTGGATCCACCGGAGCGCGGGAGCCCGCCAGACCTTC 60
Db 834 TACTCCGAGTCTCCGGGTGTGGATCCACCGGAGCGCGGGAGCCCGCCAGACCTTC 893
OY 61 TACCTGGGAGAACCCCAAGGCGCCTTTACCAAAATCCCGCGGGTGGATCCGGGAGG 120
Db 894 TACCTGGGAGAACCCCAAGGCGCCTTTACCAAAATCCCTGCGGGTGGATCCGGGAGG 953
OY 121 CGAGGCTGGTGGGCGGGGTGACCGAGGGGGTGGGGCCAGGTTTCACACCTTCAGTG 180
Db 954 CGAGGCTGGTGGGCGGGGTGACCGAGGGGGTGGGGCCAGGTTTCATATCCTTCAGTG 1013
OY 181 GATGATTGGGTGAGCTGGGAGTCCGACGAGGAGCCCTCCCGGGGTATGAAACAGTATGC 240
Db 1014 GATGATTGGGTGAGCTGGGAGTCCGACGAGGAGCCCTCCCGGGGTATGAAACAGTATGC 1073
OY 241 CTACGATGGCAAGGATTACCTGCGCTGGAACGAGACTGCGCTCTGTGACCGCAGCAGCA 300
Db 1074 CTACGATGGCAAGGATTACCTGCGCTGGAACGAGACTGCGCTCTGTGACCGCAGCAGCA 1133
OY 301 CACTGGGCTCAGATTCACAAGGCGCAAGTGTGAGCGGCGCAATGTGGCAACAAAGAG 360
```



Db 1134 CACTGGGCTCAGATCTCCAGGCGCAAGTGTAGGGCGCCAAATGTCCTGAACAAAGAG 1193  
QY 361 AGCCTACCTGAGAGGACAGTGGTGGAGTGGCTCCACAGATACCTGAGAAAGGAGAGA 420  
Db 1194 AGCCTACCTGAGAGGACAGTGGTGGAGTGGCTCCACAGATACCTGAGAAAGGAGAGA 1253  
QY 421 GATGCTGACAGCGCGGGGTACCAAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 480  
Db 1254 GATGCTGACAGCGCGGGGTACCAAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 1313  
QY 481 CTCAGCTGGCCTTACACAGAGAGAGAGAAATGGAGCCAACTAGATATATGCCCT 540  
Db 1314 CCCAGCTGGCCTTACACAGAGAGAGAGAAATGGAGCCAACTAGATATATGCCCT 1373  
QY 541 CCCTGTGCTCTGAGAGAGAGAAATCTCTGGTTCCTGATCTCTGATACCAAGAGTGA 600  
Db 1374 CCCTGTGCTCTGAGAGAGAGAAATCTCTGGTTCCTGATCTCTGATACCAAGAGTGA 1433  
QY 601 TTCCTGAGGGCCGCTCCCTGCTCTGTGGACAAATTAAAGGATGAAGTCTGTAGGGAGTGA 660  
Db 1434 TTCCTGAGGGCCGCTCCCTGCTCTGTGGACAAATTAAAGGATGAAGTCTGTAGGGAGTGA 1493  
QY 661 GGGGAAGAACATCCCTGGAGAACTGATCAGGGGTTCCCTTTAGCCCCACAGAGCCTTGG 720  
Db 1494 GGGGAAGAACATCCCTGGAGAACTGATCAGGGGTTCCCTTTGACCCACAGAGCCTTGG 1553  
QY 721 CACAGAGACTTTCCCTCAGAGCCTTTGTTCTCTGCTCACACTCAATGTTGGGGGTC 780  
Db 1554 CACAGAGACTTTCCCTCAGAGCCTTTGTTCTCTGCTCACACTCAATGTTGGGGAGTTC 1613  
QY 781 TGACTCCAGCTCTCTGAGTCCCTTGGCCTCCACTCAGTCAAGAACCGGAGGTCCTCTCT 840  
Db 1614 TGACTCCAGCTCTCTGAGTCCCTTGGCCTCCACTCAGTCAAGAACCGGAGGTCCTCTCT 1673  
QY 841 CCCCCGCTCAGAGACTAGAACTTTCCAAAGAGATAGAGATTTTCCAGAGTGGCCGTGCC 900  
Db 1674 CCCCCGCTCAGAGACTAGAACTTTCCAAAGAGATAGAGATTTTCCAGAGTGGCCGTGCC 1733  
QY 901 AGGCTGTGTCTGGGTTCTGTGCTCCCTTCCACCCAGTAGTATGTGTTCTTTTAAAG 960  
Db 1734 AGGCTGTGTCTGGGTTCTGTGCTCCCTTCCACCCAGTAGTATGTGTTCTTTTAAAG 1793  
QY 961 ATGTTCACATCCAGGTCCTGTGTGAGTGTCCCATGAGAGATGCAAAAGTCTTGAATTTTC 1020  
Db 1794 ATGTTCACATCCAGGTCCTGTGTGAGTGTCCCATGAGAGATGCAAAAGTCTTGAATTTTC 1853  
QY 1021 TGACTCTTCCTTTCAGACCCCCCAAGACACACGTGACCCACACCCCTGTCTTACTAT 1080  
Db 1854 TGACTCTTCCTTTCAGACCCCCCAAGACACACGTGACCCACACCCCTGTCTTACTAT 1913  
QY 1081 GAGGCTACCCCTGAGTGTCTGGGCTTCTACCCCTGGGAGATCATACTGACTGG 1140  
Db 1914 GAGGCTACCCCTGAGTGTCTGGGCTTCTACCCCTGGGAGATCATACTGACTGG 1973  
QY 1141 CAGCGGATGGGAGAGACCAAGACAGAGCTGTGAGCTGTGAGAGACCAAGGCTTCAGGG 1200  
Db 1974 CAGCGGATGGGAGAGACCAAGACAGAGCTGTGAGAGCTGTGAGAGACCAAGGCTTCAGGG 2033  
QY 1201 GATGGAACCTTCCAGAAAGTGGGACCTGTGTGTGCTTCTTGAGAGAGAGAGAGATAC 1260  
Db 2034 GATGGAACCTTCCAGAAAGTGGGACCTGTGTGTGCTTCTTGAGAGAGAGAGAGATAC 2093  
QY 1261 AGCTGCATGTGACAGATGAGGGGCTGCCGAGAGCCCTCATGCTAGATGAGTAAGAG 1320  
Db 2094 AGCTGCATGTGACAGATGAGGGGCTGCCGAGAGCCCTCATGCTAGATGAGTAAGAG 2153  
QY 1321 GGAGATGAGGAGCATGTCTGTAAAGGAAGCAGAGAGCCTCTGGAAGACCTTTAAACAG 1380  
Db 2154 GGAGATGAGGAGCATGTCTGTAAAGGAAGCAGAGAGCCTCTGGAAGACCTTTAAACAG 2213  
QY 1381 GGTGGTGTGTGAGGCTGGGGGTACAGAGACCTCACCTTTCACCTCTTCCAGAGCAGT 1440  
Db 2214 GGTGGTGTGTGAGGCTGGGGGTACAGAGACCTCACCTTTCACCTCTTCCAGAGCAGT 2273

QY 1441 CTTCCTTGCCACCACATCCCATATGGGATACGTGTGCTGGCCTGTGTCTTGCACCTG 1500  
Db 2274 CTTCCTTGCCACCACATCCCATATGGGATACGTGTGCTGGCCTGTGTCTTGCACCTG 2333  
QY 1501 TAGTCACTGAGAGCTGGGTCGCTCTGTGTGTGAGAAAGAGAGCTCAGTTAAGAGAG 1560  
Db 2334 TAGTCACTGAGAGCTGGGTCGCTCTGTGTGTGAGAAAGAGAGCTCAGTTAAGAGAG 2393  
QY 1561 GCGTGACAGTGGGGTCTGAATTTTCTTGTCCACTGGGGGTTTCAAGCCCCACAGTGAAG 1620  
Db 2394 GCGTGACAGTGGGGTCTGAATTTTCTTGTCCACTGGGGGTTTCAAGCCCCACAGTGAAG 2453  
QY 1621 GTGTGCCCTGCTGTTACTTGGAGACCAATCCACACTATGGAGCCCTACCCAGCCGGG 1680  
Db 2454 GTGTGCCCTGCTGTTACTTGGAGACCAATCCACACTATGGAGCCCTACCCAGCCGGG 2513  
QY 1681 CCTGTGTGCCAGACCTTCTCTTTGTAAAGCACCTGTGACAAATGAAGAGACAGATTAT 1740  
Db 2514 CCTGTGTGCCAGACCTTCTCTTTGTAAAGCACCTGTGACAAATGAAGAGACAGATTAT 2573  
QY 1741 TACCTTGATGATGTAGTGAATGGGACCTGATCCCAATATCACAGGTCAAGAGAGTTC 1800  
Db 2574 CACCTTGATGATGTAGTGAATGGGACCTGATCCCAATATCACAGGTCAAGAGAGAGTTC 2633  
QY 1801 CCTGGCTPAGAGACAGACCTTAGAGAGGACAGTGGTCGAGAGCCACATCTGCTTCCCTTG 1860  
Db 2634 CCTGGCTPAGAGACAGACCTTAGAGAGGACAGTGGTCGAGAGCCACATCTGCTTCCCTTG 2693  
QY 1861 TTTTTCCTGAT - CGCCCTGGGCTGTGACATCACAAATTTCTGAAACTTCTCGAGGGTCC 1918  
Db 2694 TTTTTCCTGATCGCCCTGTGTGACATCACAAATTTCTGAAACTTCTCGAGGGTCC 2753  
QY 1919 AAGACTAGAGAGTTCCTGTAGAGACCTATGGCCCTGGCACCTTTCTGGCTTCACAGGA 1978  
Db 2754 AAGACTAGAGAGTTCCTGTAGAGACCTATGGCCCTGGCACCTTTCTGGCTTCACAGGA 2813  
QY 1979 CATTTTCTCCACAGATTGAAAGGAGGAGAGTACTCAGGCTGCAAGTAAAGTATGAA 2038  
Db 2814 CGTTTCTTCCACAGATTGAAAGGAGGAGAGTACTCAGGCTGCAAGTAAAGTATGAA 2873  
QY 2039 GAGAGCTGATCCCTGAGATCCCTGGGATCTTGTGTTGGAGGCCATGSGGAGCTCACCC 2098  
Db 2874 GAGAGCTGATCCCTGAGATCCCTGGGATCTTGTGTTGGAGGCCATGSGGAGCTCACCC 2933  
QY 2099 ACCCCACAATTCCTCTCTGGCCACATCTCTGTGGTCTGTGACCAAGTCTGTGTTTGT 2158  
Db 2934 ACCCCACAATTCCTCTCTGGCCACATCTCTGTGGTCTGTGACCAAGTCTGTGTTTGT 2993  
QY 2159 TCTACTGACGACATGACAGAGGCCAGGGCTCTAATGTGTCTCAGGGCTTGAATGT 2218  
Db 2994 TCTACTGACGACATGACAGAGGCCAGGGCTCTAATGTGTCTCAGGGCTTGAATGT 3053  
QY 2219 GACACCCCGGGGGGCTGATGTGTGTGGGTTGTGAGGGGAAACAGGGGACATAGCTGTGC 2278  
Db 3054 GACACCCCGGGGGGCTGATGTGTGTGGGTTGTGAGGGGAAACAGTGCATAGCTGTGC 3113  
QY 2279 TATGAGTTCCTTGTGACTTCAATGTATTTGAGCAATGTATGGGCTGTTAAAGTTCACCC 2338  
Db 3114 TATGAGTTCCTTGTGACTTCAATGTATTTGAGCAATGTATGGGCTGTTAAAGTTCACCC 3173  
QY 2339 CTCACGTGACGTATGAAATTTTGTATGAAATTTTCTGTAGTGAAGAGAGCTGCC 2398  
Db 3174 CTCACGTGACGTATGAAATTTTGTATGAAATTTTCTGTAGTGTGAAGAGAGCTGCC 3233  
QY 2399 CTGTGTGGAGCTGAGTGGCAAGATTTGTCAATGCCCTTCCCTTTG 2442  
Db 3234 CTGTGTGGAGCTGAGTGGCAAGATTTGTCAATGCCCTTCCCTTTG 3277

RESULT 8  
AC004193/c AC004193 38194 bp DNA linear PRI 08-DEC-1998  
LOCUS

DEFINITION Homo sapiens clone UWGC:Y23c142 from 6p21, complete sequence.  
AC004193  
VERSION AC004193.1 GI:3980471  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Janer M., Guillaudoux T., Vu O., Kuyavin T., Harter H. and  
Geraghty D.E.  
TITLE Large scale sequence analysis of the human MHC class I region  
JOURNAL Unpublished (1998)  
REMARK Fred Hutchinson Cancer Research Center  
The Clinical Research Division  
1100 Fairview Ave. N., P.O. Box 19024  
Seattle, WA 98109-1024  
2 (bases 1 to 38194)  
Geraghty, D.E. and Olson, M.V.  
REFERENCE Direct Submission  
AUTHORS Submitted (23-FEB-1998) Human Genome Center, University of  
JOURNAL Washington, Box 352145, Seattle, WA 98195, USA  
TITLE 3 (bases 1 to 38194)  
AUTHORS Geraghty, D.E. and Olson, M.V.  
REFERENCE Direct Submission  
JOURNAL Submitted (08-DEC-1998) Human Genome Center, University of  
Washington, Box 352145, Seattle, WA 98195, USA  
TITLE University of Washington Human Genome Center  
REMARK Box 352145 Seattle, WA 98195  
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)  
On Dec 8, 1998 this sequence version replaced g1:2905867.  
Overlapping Sequences:  
5': UWGC:Y23C022 (Genbank Accession: AC004194)  
3': UWGC:Y23X010 (Genbank Accession: AC004172)  
-----  
Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
Genbank flat file format but are available as part  
of this entry's ASN.1 file.  
-----  
Double stranded (DS) coverage: 90.7%  
DS or two chemistry coverage: 100.0%  
Single stranded regions: 0  
-----  
Sequence Validation:  
This sequence has been validated by Multiple Complete Digest  
Mapping. Comparison of the experimentally derived map digest  
fragments with sequence-predicted fragments is given below.  
Small fragments below a variable cutoff (approximately 400-600bp)  
are not mapped and hence do not appear in the table. There are no  
significant remaining discrepancies between the experimental and  
predicted values. Uniquely ordered fragment groups are separated  
by dashed lines.  
-----  
Map BgIII Seq HindIII Seq NsiI Seq  
-----  
3121.81 3124.00 2611.88 2559.00 1668.32 1694.00  
-----  
6992.92 6962.00 2803.45 2806.00 2697.65 2688.00  
-----  
2418.71 2395.00 5412.37 5370.00 5391.17 5365.00  
-----  
1445.83 1463.00 7334.90 7251.00 1767.38 1763.00  
-----  
4617.62 4628.00 513.70 507.00 1664.00 1666.00  
-----  
11708.00 11842.00 1572.62 1604.00 2239.00 2203.00  
-----

FEATURES  
source  
-----  
Location/Qualifiers  
1. 38194  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/map="6p21"  
/clone="CGM1:A190C8"  
/sub\_clone="UWGC:Y23c142"  
/cell\_line="CGM1"  
/clone\_id="Wash U YAC Library"  
/complement(322..612)  
/rpl\_family="Alu"  
complement(4079..4376)  
/rpl\_family="Alu"  
complement(4672..5947)  
/rpl\_family="L1"  
complement(6045..6157)  
/rpl\_family="Alu"  
complement(6453..6760)  
/rpl\_family="Alu"  
complement(7699..7796)  
/rpl\_family="L1"  
complement(8600..8736)  
/rpl\_family="Alu"  
complement(16938..17060)  
/rpl\_family="MLT1"  
17202..17458  
/rpl\_family="LTR10"  
18575..18862  
/rpl\_family="Alu"  
19242..19518  
/rpl\_family="Alu"  
complement(22650..22763)  
/rpl\_family="Alu"  
complement(23124..23374)  
/rpl\_family="Alu"  
23637..23904  
/rpl\_family="Alu"  
23942..24393  
/rpl\_family="MLT2B2"  
complement(25520..25994)  
/rpl\_family="L1"  
complement(26071..26359)  
/rpl\_family="Alu"  
complement(26565..26672)  
/rpl\_family="L1"  
complement(28309..28449)  
/rpl\_family="MER20"  
29016..29140  
/rpl\_family="Alu"  
30585..30812  
/rpl\_family="MER30"  
31405..31685  
/rpl\_family="Alu"  
complement(37038..37232)  
/rpl\_family="Alu"  
38017..38191  
/rpl\_family="Alu"  
-----  
BASE COUNT 10141 a 8406 c 8306 g 11341 t  
ORIGIN  
-----  
Query Match 98.1% Score 2395.4; DB 9; Length 38194;  
Best Local Similarity 99.8% Pred. NO. 0;  
Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY	1	TACTCCCGAGTCTCGGGTCTBGGATCCACC	CGAGGCGCGGAGACCGCCACGACCTTC	60
Db	34752	TACTCCCGAGTCTCGGGTCTBGGATCCACC	CGAGGCGCGGAGACCGCCACGACCTTC	346933
QY	61	TACTCCGGAGAACCCCAAGGGCCCTTTCACAAAT	CCCCGGGGTGGTCCGGGCGAGCCTC	120
Db	34692	TACTCCGGAGAACCCCAAGGGCCCTTTCACAAAT	CCCCGGGGTGGTCCGGGCGAGCCTC	346333
QY	121	CGAGGCTCGGTGGGCGGGGCTGACGAGAGGGG	TGGGGCAGGTTCCTACACCTCCAGTG	180
Db	34632	CGAGGCTCGGTGGGCGGGGCTGACGAGAGGGG	TGGGGCAGGTTCCTACACCTCCAGTG	345733
QY	181	GATGATTTGGCTGCGACTTGGGCTCCGACGAGC	CGCTCTCCGGGGTATGACATATGC	240
Db	34572	GATGATTTGGCTGCGACTTGGGCTCCGACGAGC	CGCTCTCCGGGGTATGACATATGC	345133
QY	241	CTACGATTTGGCAGATTAACCTGGCCCTACAGAG	AGGACTGGCTGCTCGACCGCAGCGA	300
Db	34512	CTACGATTTGGCAGATTAACCTGGCCCTACAGAG	AGGACTGGCTGCTCGACCGCAGCGA	344533
QY	301	CACGCGGCTCAATCTCCAAACGCAAGTGTAGG	CGGCGCAATGTGCTCAACAAAGAG	360
Db	34452	CACGCGGCTCAATCTCCAAACGCAAGTGTAGG	CGGCGCAATGTGCTCAACAAAGAG	343933
QY	361	AGCCTACTGGAGGGGACGTGGCTGGAGTGGCTC	CACAGATACCTGGAGAGAGGGAAGA	420
Db	34392	AGCCTACTGGAGGGGACGTGGCTGGAGTGGCTC	CACAGATACCTGGAGAGAGGGAAGA	343333
QY	421	GATGTCTCAGACGGGGGTACCGAGGGGCAGTGG	GGGCGCTCCTCGATCTCCTGAACCT	480
Db	34332	GATGTCTCAGACGGGGGTACCGAGGGGCAGTGG	GGGCGCTCCTCGATCTCCTGAACCT	342733
QY	481	CTCAGCCTGGCTCAGACAAAGAGAGAGAAAT	GGGACCAACATCAGAAATATCGCCCT	540
Db	34272	CTCAGCCTGGCTCAGACAAAGAGAGAGAAAT	GGGACCAACATCAGAAATATCGCCCT	342133
QY	541	CCCTCTGGTCTGAGGAGAGAGAAATCTCTGGG	TTTCCAGATCTGTACAGAGGTGA	600
Db	34212	CCCTCTGGTCTGAGGAGAGAGAAATCTCTGGG	TTTCCAGATCTGTACAGAGGTGA	341533
QY	601	TTTCTGAGGGGCCCTCTGCTCTCTGGGACAAAT	TAAAGGATGAATCTCTGAGGAGTGA	660
Db	34152	TTTCTGAGGGGCCCTCTGCTCTCTGGGACAAAT	TAAAGGATGAATCTCTGAGGAGTGA	340933
QY	661	GGGGAACACAAATCCCTGGAAAGACTGATCGAG	GGGCTCCCTTGAGCCCAACAGACCTGG	720
Db	34092	GGGGAACACAAATCCCTGGAAAGACTGATCGAG	GGGCTCCCTTGAGCCCAACAGACCTGG	340333
QY	721	CACGAGACCTTTTCCCTCAGGCGCTTGTCTCTG	CCCTACACATGATGTGTGGGGGTC	780
Db	34032	CACGAGACCTTTTCCCTCAGGCGCTTGTCTCTG	CCCTACACATGATGTGTGGGGGTC	339733
QY	781	TGACTCCAGTCTCTGATGTCCTTGGGCTCCACT	CAAGTACAGACCGAGAGTCCCTGCT	840
Db	33972	TGACTCCAGTCTCTGATGTCCTTGGGCTCCACT	CAAGTACAGACCGAGAGTCCCTGCT	339133
QY	841	CCCCGCTCAGAGACATAGAACTTCCAAACGAT	TAGAGATTAATCCGAGTGGCCGTGTC	900
Db	33912	CCCCGCTCAGAGACATAGAACTTCCAAACGAT	TAGAGATTAATCCGAGTGGCCGTGTC	338533
QY	901	AGGCTGGTGTCTGGGTCTGTGCTCCCTTCCAC	CGCCAGGTATCTGGTTCATTCCTAGG	960
Db	33852	AGGCTGGTGTCTGGGTCTGTGCTCCCTTCCAC	CGCCAGGTATCTGGTTCATTCCTAGG	337933
QY	961	ATGGTCAATCAGAGTCTGCTGGAGTGTCCATGAG	AGATGCAAAAGTCTTGAAATTTTC	1020
Db	33792	ATGGTCAATCAGAGTCTGCTGGAGTGTCCATGAG	AGATGCAAAAGTCTTGAAATTTTC	337333
QY	1021	TGACGCTTTCCTTTACAGCCCCCCCCAAGACAG	ACAGAGTACCACACCGCTTGTGACTAT	1080
Db	33732	TGACGCTTTCCTTTACAGCCCCCCCCAAGACAG	ACAGAGTACCACACCGCTTGTGACTAT	336733
QY	1081	GAGGCGACCCCTGAGGTCTGGGCGCTTGGGCT	CTTCAACCTGGGAGATCATCTGACTGG	1140

D	b	33672	GAGGCGACCCCTGAGGTGCTGGGCGCTGGAGCTTCTACCCCTGGGAGATATACTGACCTGG	33613
Q	y	1141	CAGCGGAGTGGGGAGGAGACAGACCCAGAGACGGAGCTCTGGAGAGACCAGGCTTCAGAG	1200
D	b	33612	CAGCGGAGTGGGGAGGAGACAGACCCAGAGACGGAGCTCTGGAGAGACCAGGCTTCAGAG	33553
Q	y	1201	GATGGACCTTCAGAAAGTGGGCGAGCTGTGGTGTGCTTCGGAGAGAGCAGAGATTAC	1260
D	b	33552	GATGGACCTTCAGAAAGTGGGCGAGCTGTGGTGTGCTTCGGAGAGAGCAGAGATTAC	33493
Q	y	1261	ACGTCGCATGTGCACGATGAGGGGCTGCCGGAGCCCTCATGTCTAAGATGGAGTAAGAG	1320
D	b	33492	ACGTCGCATGTGCACGATGAGGGGCTGCCGGAGCCCTCATGTCTAAGATGGAGTAAGAG	33433
Q	y	1321	GAGAGTGGAGGATATGTCTGTATGGGAAACAGAGAGCTCTCGAAGACCTTTAAACAG	1380
D	b	33432	GAGAGTGGAGGATATGTCTGTATGGGAAACAGAGAGCTCTCGAAGACCTTTAAACAG	33373
Q	y	1381	GGTCGGGTGAAGGCTGGGGGTACAGAACCTTCACCTTCCTTTCCAGAGCAGT	1440
D	b	33372	GGTCGGGTGAAGGCTGGGGGTACAGAACCTTCACCTTCCTTTCCAGAGCAGT	33313
Q	y	1441	CTTCCCTGCCACCATCCCATCATGGGTATGTGTCTGGCTGGTGTCTCTTGCAGCTG	1500
D	b	33312	CTTCCCTGCCACCATCCCATCATGGGTATGTGTCTGGCTGGTGTCTCTTGCAGCTG	33253
Q	y	1501	TAGTCACGTGGAGCTGGGGCTGGCTGTGTCTGTGGAAAGAGAGCTCAGGTAAAGAG	1560
D	b	33252	TAGTCACGTGGAGCTGGGGCTGGCTGTGTCTGTGGAAAGAGAGCTCAGGTAAAGAG	33193
Q	y	1561	GGGTGACAAAGTGGGGTCTAGATTCTTCTGTCCACTGGGGGTTTCAAGCCCGAGTAGAA	1620
D	b	33192	GGGTGACAAAGTGGGGTCTAGATTCTTCTGTCCACTGGGGGTTTCAAGCCCGAGTAGAA	33133
Q	y	1621	GTGTGCCCTGCTGGTGTACTGGGAAGCACCATCCACACTCATGGGCTTACCGAGCTGGG	1680
D	b	33132	GTGTGCCCTGCTGGTGTACTGGGAAGCACCATCCACACTCATGGGCTTACCGAGCTGGG	33073
Q	y	1681	CGCTGTGTCCAGACACCTCTCTTTTGTAAACACACTGTGAACATGAAGAGACAGATTAT	1740
D	b	33072	CGCTGTGTCCAGACACCTCTCTTTTGTAAACACACTGTGAACATGAAGAGACAGATTAT	33013
Q	y	1741	TACCTTGATGATGTAGTATGGGAGCCGATCCGAGTATACAGAGTCAAGAGAGATC	1800
D	b	33012	TACCTTGATGATGTAGTATGGGAGCCGATCCGAGTATACAGAGTCAAGAGAGATC	32953
Q	y	1801	CCTGGCTAAGACAGACCTTAGAGAGGGCAGTTGTGAGAGACCCACATCTGCTTTCCTTG	1860
D	b	32952	CCTGGCTAAGACAGACCTTAGAGAGGGCAGTTGTGAGAGACCCACATCTGCTTTCCTTG	32893
Q	y	1861	TTTTTTCCTAT--CGCCCGGGGTGTGCATGCACACATTTCTGAAACCTTCTGAGGGTCC	1918
D	b	32892	TTTTTTCCTATCCCGCCCGGGGTGTGCATGCACACATTTCTGAAACCTTCTGAGGGTCC	32833
Q	y	1919	AAGACTAGAGAGTTCCTCTAGGACCTCAAGGCGCTCCGACCTTTCGTGGCCTTCACAGGA	1978
D	b	32832	AAGACTAGAGAGTTCCTCTAGGACCTCAAGGCGCTCCGACCTTTCGTGGCCTTCACAGGA	32773
Q	y	1979	CATTTTCTTCCACAGATTGAAAGAGGGAGGAGCTACTCTCAGGCTGCAGATGAATGAA	2038
D	b	32772	CATTTTCTTCCACAGATTGAAAGAGGGAGGAGCTACTCTCAGGCTGCAGATGAATGAA	32713
Q	y	2039	GGAGGCTGATCCCTGAGATCTTTGGGATCTTGTGTGGAG--CCATGGGGGAGGCTCAC	2097
D	b	32712	GGAGGCTGATCCCTGAGATCTTTGGGATCTTGTGTGGAGCCCATGGGGAGGCTCAC	32653
Q	y	2098	CACCCACATTTCTCTCTGGCCACATCTCGTGTGTCTGACACAGTGTCTGTTTTG	2157
D	b	32652	CACCCACATTTCTCTCTGGCCACATCTCGTGTGTCTGACACAGTGTCTGTTTTG	32593
Q	y	2158	TTCTACTTAGGACGTGACAGTGCACGAGGCTCTAATGTGTCTTCACGGCTTGAATG	2217

Db 32392 TTCTACTCTAGGACGATGACGTCGCCAGGCGCTCAATGTGTCTCTCAGCGCTGTAAATG 32333  
QY 2218 TGACACCCCGGGGGCCCTGATGTGTGTGGTGTGAGGGGACAGGGACATAGCTGTG 2277  
Db 32532 TGACACCCCGGGGGCCCTGATGTGTGTGGTGTGAGGGGACAGGGACATAGCTGTG 32473  
QY 2278 CTATGAGGTTCTTGTGACCTCAATGTATTTGAGCATGTGATGGGCGTTTAAAGTGTACC 2337  
Db 32472 CTATGAGGTTCTTGTGACCTCAATGTATTTGAGCATGTGATGGGCGTTTAAAGTGTACC 32413  
QY 2338 CCTGACGTGACATATGATATTTGTTTCATCATATTTTCTGTAGTGTGAACAGCTGC 2397  
Db 32412 CCTGACGTGACATATGATATTTGTTTCATCATATTTTCTGTAGTGTGAACAGCTGC 32353  
QY 2398 CCTGTGTGGAGCTAGTGGCAG 2420  
Db 32352 CCTGTGTGGAGCTAGTGGCAG 32330

RESULT 9  
AL645929/c  
LOCUS Human DNA sequence from clone Xxbac-1216 on chromosome 6, complete  
DEFINITION sequence.  
ACCESSION AL645929  
VERSION AL645929.3 GI:18072572  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Griffiths, C.  
TITLE Direct Submision  
JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Jan 6, 2002 this sequence version replaced gi:11736625.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em, EMBL; Sw,  
SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C-elegans/wormpep/xbac-1216-1s  
from a CHORI-501 human bac - PGF cell line library VECTOR:  
PTARPA2.1

FEATURES  
source  
1. 93937  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="Xxbac-1216"  
/clone\_lib="CHORI-501"  
24784 a 20804 c 21255 g 27094 t  
http://www.sanger.ac.uk/HGP/Chf6/MHC.  
Location/Qualifiers

BASE COUNT 24784 a 20804 c 21255 g 27094 t  
ORIGIN

Query Match

98.1%; Score 2395.4; DB 9; Length 93937;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;  
QY 1 TACTCCGAGTCTCCGGGTCTGGGATCCACCCGAGCGCGGGACCCGACACCTC 60  
Db 76937 TACTCCGAGTCTCCGGGTCTGGGATCCACCCGAGCGCGGGACCCGACACCTC 76878  
QY 61 TACCTGGGAGAACCCCAAGGGCGCTTACCAAAATCCCCGGGGGTCCGGCGAGG 120  
Db 76877 TACCTGGGAGAACCCCAAGGGCGCTTACCAAAATCCCCGGGGGTCCGGCGAGG 76818  
QY 121 CGAGGCTCGTGGCGGGGCTGACCGAGGGGGTGGGCGCAGTTCTCCACCTCCAGT 180  
Db 76817 CGAGGCTCGTGGCGGGGCTGACCGAGGGGGTGGGCGCAGTTCTCCACCTCCAGT 76758  
QY 181 GATGATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCGCGGGATGGAACAGTATGC 240  
Db 76757 GATGATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCGCGGGATGGAACAGTATGC 76698  
QY 241 CTACGATGGCAAGATTAACCTTCGCGCTGAAAGAGAGACTGCGCTCTGTGACCGACGCGA 300  
Db 76697 CTACGATGGCAAGATTAACCTTCGCGCTGAAAGAGAGACTGCGCTCTGTGACCGACGCGA 76638  
QY 301 CACTGCGGCTCAGATCTCCACAGCGCAAGTCTGAGGCGGCCAATGTGGCTGAACAAGAGAG 360  
Db 76637 CACTGCGGCTCAGATCTCCACAGCGCAAGTCTGAGGCGGCCAATGTGGCTGAACAAGAGAG 76578  
QY 361 AGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAACGGGAAGA 420  
Db 76577 AGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAACGGGAAGA 76518  
QY 421 GATGCTGAGGCGCGGGTACCAAGGGCAGTGGGGCGCTCCCGATCTCTGTAGACT 480  
Db 76517 GATGCTGAGGCGCGGGTACCAAGGGCAGTGGGGCGCTCCCGATCTCTGTAGACT 76458  
QY 481 CTCAGCTGGGCTAGCAACAGAGAGAGAGAAATGGGACCAACTAGAAATATGCGCCT 540  
Db 76457 CTCAGCTGGGCTAGCAACAGAGAGAGAGAAATGGGACCAACTAGAAATATGCGCCT 76398  
QY 541 CCCCTGTGCTTGAGGAGAGAGAAATCTCTGCGGTTTCCAGATCTGTACAGAGACTGA 600  
Db 76397 CCCCTGTGCTTGAGGAGAGAGAAATCTCTGCGGTTTCCAGATCTGTACAGAGACTGA 76338  
QY 601 TTTCGAGGCGCGGCTCGCTGTCGTCGAGCAATTAAGGATGAATCTGTAGGGAGTGA 660  
Db 76337 TTTCGAGGCGCGGCTCGCTGTCGTCGAGCAATTAAGGATGAATCTGTAGGGAGTGA 76278  
QY 661 GGGGAGACAAATCCCTGGAAGACTGATCAGGGGTTCCCTTTGACCCCAAGACAGCTTGG 720  
Db 76277 GGGGAGACAAATCCCTGGAAGACTGATCAGGGGTTCCCTTTGACCCCAAGACAGCTTGG 76218  
QY 721 CACGAGACATTTTCCCTCAGAGCTTTTCTGTGCTCCACACTCATATGTGTGGGGTTC 780  
Db 76217 CACGAGACATTTTCCCTCAGAGCTTTTCTGTGCTCCACACTCATATGTGTGGGGTTC 76158  
QY 781 TGACTCCAGCTCCCTGAGTCCCTTGCGCTCCACTCAGGTGAGAGCGGAGTCCGCT 840  
Db 76157 TGACTCCAGCTCCCTGAGTCCCTTGCGCTCCACTCAGGTGAGAGCGGAGTCCGCT 76098  
QY 841 CCCCGCTCAGAGACTGGAATTTTCCAAAGAAATAGAGATTTATCCAGTGGCCGTGCC 900  
Db 76097 CCCCGCTCAGAGACTGGAATTTTCCAAAGAAATAGAGATTTATCCAGTGGCCGTGCC 76038  
QY 901 AGGCTGTGCTGTGGGTTCTGTCTCCCTTCCCAACCCAGATATGTGTTCAATTTAGG 960  
Db 76037 AGGCTGTGCTGTGGGTTCTGTCTCCCTTCCCAACCCAGATATGTGTTCAATTTAGG 75978  
QY 961 ATGGTCAATCCAGGTCGTCTGAGTGTCCCATGAGAGATGAAGTGTGTAATTTTC 1020  
Db 75977 ATGGTCAATCCAGGTCGTCTGAGTGTCCCATGAGAGATGAAGTGTGTAATTTTC 75918  
QY 1021 TGACTCTTCCTTCAGACCCCGCCCAAGACACAGTGAACCCACACCTGTCTTTGACTAT 1080  
|||||

Db 75917 TGACTCTTCCCTTTAGACCCCCCAAGACACAGCTGACCCACACCCCTGCTCTTTCATAT 75858  
OY 1081 GAGGCCACCTTGAGGTGCTGGGCCCTTACCTCTGGGAGATCATCTGACCTGG 1140  
Db 75857 GAGGCCACCTTGAGGTGCTGGGCCCTTACCTCTGGGAGATCATCTGACCTGG 75798  
OY 1141 CAGCGGATGGGGAGGAGACACAGCCAGAGCTGAGCTGTGGAGACCAGGCTTCAGAG 1200  
Db 75797 CAGCGGATGGGGAGGAGACACAGCCAGAGCTGTGGAGACCAGGCTTCAGAG 75738  
OY 1201 GATGGAACCTTCAGAAATGGGAGCTGTGTGGCTTCTTGGAGAGACAGAGATAC 1260  
Db 75737 GATGGAACCTTCAGAAATGGGAGCTGTGTGGCTTCTTGGAGAGACAGAGATAC 75678  
OY 1261 AGCTGCATGTGCACATGAGGGGCTGCCGAGCCCTCATGCTGAGATGGAGTAAGAG 1320  
Db 75677 AGCTGCATGTGCACATGAGGGGCTGCCGAGCCCTCATGCTGAGATGGAGTAAGAG 75618  
OY 1321 GGAGATGAGGAGCATATGCTGTAGGAAAGCAGAGACCTCTGTGAAGACCTTTAACAG 1380  
Db 75617 GGAGATGAGGAGCATATGCTGTAGGAAAGCAGAGACCTCTGTGAAGACCTTTAACAG 75558  
OY 1381 GGTGCTGTGTAGGGCTGGGGGCTGAGAGACCTCATCTTCACTCTCTCCACAGCAGT 1440  
Db 75557 GGTGCTGTGTAGGGCTGGGGGCTGAGAGACCTCATCTTCACTCTCTCCACAGCAGT 75498  
OY 1441 CTTCCTGCTCCACCATATCCCATCATGAGGTATGCTGTGGCTGGTGTGCTTCCAGAGCTG 1500  
Db 75497 CTTCCTGCTCCACCATATCCCATCATGAGGTATGCTGTGGCTGGTGTGCTTCCAGAGCTG 75438  
OY 1501 TAGTCATGAGAGCTGGGTGCTGCTGTGCTGTGGAGAAAGAGAGCTCAGGTAAGAG 1560  
Db 75437 TAGTCATGAGAGCTGGGTGCTGCTGTGCTGTGGAGAAAGAGAGCTCAGGTAAGAG 75378  
OY 1561 GGGTACACAGTGGGGTCTGAGTTTCTTGTCTCCACTGGGGGTTTCAAGCCAGGTACAA 1620  
Db 75377 GGGTACACAGTGGGGTCTGAGTTTCTTGTCTCCACTGGGGGTTTCAAGCCAGGTACAA 75318  
OY 1621 GTGTCCCTGCTGTGTACTGGAGACACATCCACTCATGTGGGCTTACCAGGCTGGG 1680  
Db 75317 GTGTCCCTGCTGTGTACTGGAGACACATCCACTCATGTGGGCTTACCAGGCTGGG 75258  
OY 1681 CCCTGTGTGCCAGACCTTCTCTTTTGTAAAGCAGCTGTGACATGAAGACAGATTTAT 1740  
Db 75257 CCCTGTGTGCCAGACCTTCTCTTTTGTAAAGCAGCTGTGACATGAAGACAGATTTAT 75198  
OY 1741 TACCTGTAGATGTAGAGATGGGGAGCTGATCCAGTAATCACAGGCTCAGAGAAAGTTC 1800  
Db 75197 TACCTGTAGATGTAGAGATGGGGAGCTGATCCAGTAATCACAGGCTCAGAGAAAGTTC 75138  
OY 1801 CCTGGCTAAGGACAGACCTTGAAGAGGAGTGTGTCGAGAGCCACATCTGCTTCTCTTG 1860  
Db 75137 CCTGGCTAAGGACAGACCTTGAAGAGGAGTGTGTCGAGAGCCACATCTGCTTCTCTTG 75078  
OY 1861 TTTTTCCTGAT--CGCCCTGGGCTGCACTACACATTTCTGGAACCTTCTCGAGGCTC 1918  
Db 75077 TTTTTCCTGATCCGCTCGGCTGCACTACACATTTCTGGAACCTTCTCGAGGCTC 75018  
OY 1919 AAGATAGAGAGTCTCTAGAGACCTCAAGGCTGAGGCTGGCTGGCTCTACAGAGA 1978  
Db 75017 AAGATAGAGAGTCTCTAGAGACCTCAAGGCTGAGGCTGGCTGGCTCTCTACAGAGA 74958  
OY 1979 CATTTTCTCCACAGATTGAAAAGAGAGGAGCTACTCTCAGAGGCTGCAAGTAAGTAA 2038  
Db 74957 CATTTTCTCCACAGATTGAAAAGAGAGGAGCTACTCTCAGAGGCTGCAAGTAAGTAA 74898  
OY 2039 GGAGGCTGATCCCTGAGATCTTGGGATCTGTGTGGAG--CCATGGGAGAGCTACAC 2097  
Db 74897 GGAGGCTGATCCCTGAGATCTTGGGATCTGTGTGGAG--CCATGGGAGAGCTACAC 74838  
OY 2098 CACCCCAAAATTCCTCTGTGGCCACATCTCTGTGGTCTCTGACAGAGTCTGTTTTG 2157  
Db 74837 CACCCCAAAATTCCTCTGTGGCCACATCTCTGTGGTCTCTGACAGAGTCTGTTTTG 74778

OY 2158 TTCTACTAGGCGTACAGTGGCCAGGGCTCTAATGTGTCTCTCAGGCTGTAAATG 2217  
Db 74777 TTCTACTAGGCGTACAGTGGCCAGGGCTCTAATGTGTCTCTCAGGCTGTAAATG 74718  
OY 2218 TGACACCCCGGGGGGCTGATGTGTGTGGTGTGTGAGGGAGACAGGAGCATAGCTGTG 2277  
Db 74717 TGACACCCCGGGGGGCTGATGTGTGTGGTGTGTGAGGGAGACAGGAGCATAGCTGTG 74658  
OY 2278 CTATGAGCTTTCTTTGACTTCATGTATTGAGCATGTGATGGCTGTTTAAAGTCTAC 2337  
Db 74657 CTATGAGCTTTCTTTGACTTCATGTATTGAGCATGTGATGGGCTGTTTAAAGTCTAC 74598  
OY 2338 CCTCAGCTGACATGATTTGAATTTGTCATGAATATTTCTAGTGTAAACACTGTG 2397  
Db 74597 CCTCAGCTGACATGATTTGAATTTGTCATGAATATTTCTAGTGTAAACACTGTG 74538  
OY 2398 CCTGTGTGGGACTGAGTGGCAAC 2420  
Db 74537 CCTGTGTGGGACTGAGTGGCAAG 74515

RESULT 10  
HS377H14/c  
LOCUS  
DEFINITION  
Human DNA sequence from clone RP3-377H14 on chromosome 6p21.32-22.1. Contains the HLA-G gene for major histocompatibility complex class I G (HLA 6.0) an MHC class I pseudogene, an RPL7A (60S Ribosomal Protein L7A) pseudogene, a gene for a novel MHC class I protein, an interferon-inducible protein 1-80 pseudogene, an RPL23A (60S Ribosomal Protein L23A) pseudogene, an HCG1X pseudogene, an MICB or PERB1.1 pseudogene, the HLA-F gene for major histocompatibility complex class I F (CD142), and four p5-1 pseudogenes. Contains EST, STSs, GSS and six CpG islands, complete sequence.  
AL022723 GI:5002624  
VERSION  
HTG: CDA12; Cpg island; HCG1X; HLA-F; HLA-G; MICB; P5-1;  
KEYWORDS  
PERB1.1; RPL23A; RPL7A.

SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 148834)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (29-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
On Jun 7, 1999 this sequence version replaced gi:4757010.  
This sequence was generated from part of bacterial clone configs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group in collaboration with Armin Volz and Andreas Ziegler.  
Further information can be found at  
http://www.sanger.ac.uk/HGP/Ch6  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information on the WormPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep  
RP3-377H14 is from the library RPi-3 constructed by the group of Pieter de Jong.

For further details see  
<http://www.chori.org/bacpac/home.htm>  
VECTOR: PCYPAC2

This sequence is the entire insert of clone Rp3-377H14.

FEATURES  
Location/Qualifiers

source

```
1..148834
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="p21.32-22.1"
/clone="Rp3-377H14"
/clone_lib="RPCI-3"
28..179
repeat_region
/note="FAM repeat: matches 1..163 of consensus"
530..785
repeat_region
/note="AluX repeat: matches 35..290 of consensus"
1037..1314
repeat_region
/note="Aluub repeat: matches 5..293 of consensus"
1348..1799
/note="MLT2D repeat: matches 78..533 of consensus"
complement(1478..1927)
/note="match: GSS: Em:A2040015 Em:A2225799"
1487..1896
misc_feature
/note="match: GSS: Em:AL061978"
1671..1849
/note="match: GSS: Em:A2503899"
join(1700..1897,109272..109358)
/note="match: GSS: Em:AQ309390"
1700..1897
misc_feature
/note="match: GSS: Em:AQ127304"
complement(1701..1834)
/note="match: STS: Em:G27250"
1705..1900
misc_feature
/note="match: GSS: Em:AL220679"
1713..1888
misc_feature
/note="match: GSS: Em:A2329697 Em:A2515005"
complement(1719..1907)
/note="match: STS: Em:L30467"
complement(1735..1938)
/note="match: STS: Em:G12422 Em:G15742"
1735..1888
misc_feature
/note="match: GSS: Em:A2046652 Em:A2128672"
1736..1895
misc_feature
/note="match: GSS: Em:AQ082957"
1736..1880
misc_feature
/note="match: GSS: Em:AQ346974"
1737..1855
misc_feature
/note="match: STS: Em:G08015"
1739..1899
misc_feature
/note="match: GSS: Em:A2255105"
1741..2056
misc_feature
/note="match: STS: Em:G09109"
1741..1894
misc_feature
/note="match: GSS: Em:A2268990"
1745..1894
misc_feature
/note="match: GSS: Em:A2258622"
1747..1914
misc_feature
/note="match: STS: Em:G08112"
complement(1753..1893)
/note="match: STS: Em:G08713"
complement(1759..1844)
complement(1759..1844)
/note="match: STS: Em:G08342"
1761..1890
misc_feature
/note="match: GSS: Em:A2720175"
complement(1762..1922)
/note="match: GSS: Em:A2072848"
1763..1870
misc_feature
/note="match: GSS: Em:A2612907"
1763..1834
misc_feature
/note="match: STS: Em:G08619"
complement(1765..1921)
/note="match: GSS: Em:A2723231"
complement(1767..1956)
misc_feature
```

```
misc_feature
/note="match: GSS: Em:AQ631029"
complement(1767..1930)
/note="match: GSS: Em:A2436733"
1767..1906
misc_feature
/note="match: GSS: Em:A2351009"
complement(join(1768..1850,109293..109380))
/note="match: STS: Em:G08877"
complement(1768..1902)
/note="match: GSS: Em:A2445665"
complement(1768..1897)
/note="match: GSS: Em:A2652588"
complement(1768..1842)
/note="match: GSS: Em:AQ190792"
1769..1892
misc_feature
/note="match: GSS: Em:AQ756985"
join(1770..1909,105164..105297,109285..109344)
/note="match: GSS: Em:A2622312"
complement(join(1770..1901,24133..24220))
/note="match: GSS: Em:AQ231097"
1770..1922
misc_feature
/note="match: GSS: Em:AQ016311 Em:AQ565665"
1770..1902
/note="match: GSS: Em:AQ056687 Em:AQ057863"
complement(1770..1893)
/note="match: STS: Em:G15805"
1770..1888
misc_feature
/note="match: STS: Em:G09622"
join(1771..1906,109207..109358)
/note="match: GSS: Em:AQ35323"
1771..1866
misc_feature
/note="match: GSS: Em:A2860224"
1772..1902
misc_feature
/note="match: GSS: Em:AL298154"
1772..1894
misc_feature
/note="match: GSS: Em:AQ797274"
complement(join(1773..1965,109253..109369))
/note="match: GSS: Em:A2460107"
complement(join(1773..1903,109186..109344))
/note="match: GSS: Em:A2339331"
1773..1954
misc_feature
/note="match: GSS: Em:AQ094162"
1773..1939
misc_feature
/note="match: GSS: Em:A2640947"
complement(1773..1922)
/note="match: GSS: Em:AQ96755 Em:A2650375 Em:A2850525"
match: STS: Em:L30983"
complement(1773..1920)
1773..1911
misc_feature
/note="match: GSS: Em:A2849568"
1773..1911
misc_feature
/note="match: GSS: Em:A2492878"
1773..1908
misc_feature
/note="match: STS: Em:G10066"
complement(1773..1906)
/note="match: GSS: Em:A2664044"
1773..1902
misc_feature
/note="match: GSS: Em:AQ420153 Em:A2412363 Em:A2607113"
complement(1773..1902)
/note="match: GSS: Em:A2722714 Em:A2765158 Em:A2832316"
complement(1773..1900)
/note="match: STS: Em:G09956"
1773..1897
misc_feature
/note="match: GSS: Em:A2644560"
1773..1894
misc_feature
/note="match: GSS: Em:AQ55063"
complement(1773..1894)
/note="match: GSS: Em:A2581763"
complement(1773..1870)
/note="match: GSS: Em:A2490114"
complement(1773..1834)
/note="match: STS: Em:LI17665"
complement(1775..1921)
/note="match: GSS: Em:AQ984535"
1775..1907
misc_feature
```



```
/note="match: GSS: Em:A2843690"
misc_feature      1775..1906
                  /note="match: GSS: Em:A283935"
misc_feature      1775..1876
                  /note="match: GSS: Em:A2370392"

Query Match      98.1%; Score 2395.4; DB 9; Length 148834;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY      1 TACTCCGAGTCTCCGGGCTGTGGATCCACCCGAGCGCGGGAGACCCGCCAGACCTTC 60
Db      12138 TACTCCGAGTCTCCGGGCTGTGGATCCACCCGAGCGCGGGAGACCCGCCAGACCTTC 12079
QY      61 TACCTGGAGAACCCCAAGGGGCGCTTTCACAAATCCCGGGGGGTGCGGGCGAGGG 120
Db      12078 TACCTGGAGAACCCCAAGGGGCGCTTTCACAAATCCCGGGGGGTGCGGGCGAGGG 12019
QY      121 CGAGGCTCGTGGGCGGGGCTGACCGAGGGGGTGGGGCAGGTTCTCACACCTCCAGTG 180
Db      12018 CGAGGCTCGTGGGCGGGGCTGACCGAGGGGGTGGGGCAGGTTCTCACACCTCCAGTG 11959
QY      181 GATGATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGCGGGATATGAACAGTATGC 240
Db      11958 GATGATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGCGGGATATGAACAGTATGC 11899
QY      241 CTACGATGGCAAGATTACCTCGCCGCTGACGAGAGCACTGGGCGCTGAGACCGGCGGA 300
Db      11898 CTACGATGGCAAGATTACCTCGCCGCTGACGAGAGCACTGGGCGCTGAGACCGGCGGA 11839
QY      301 CACTGCGGCTCAGATCTCTCAAGCCGCAATGTGAGCGCGCAATGTGCTGAACAAAGAG 360
Db      11838 CACTGCGGCTCAGATCTCTCAAGCCGCAATGTGAGCGCGCAATGTGCTGAACAAAGAG 11779
QY      361 AGCTTACTGAGAGGACGCTGCTGAGTGGCTCCACAGATACCTGAGAAAGGGAGGA 420
Db      11778 AGCTTACTGAGAGGACGCTGCTGAGTGGCTCCACAGATACCTGAGAAAGGGAGGA 11719
QY      421 GATGCTGAGAGGCGCGGGGTACCAAGGGGCAAGTGGGGCGCTCCGATGCTCTGTAGACT 480
Db      11718 GATGCTGAGAGGCGCGGGGTACCAAGGGGCAAGTGGGGCGCTCCGATGCTCTGTAGACT 11659
QY      481 CTCAGCCTGGGCTTAGCACAGAGAGAGGAAATGGGACCAACACTAGAAATATGCGCCT 540
Db      11658 CTCAGCCTGGGCTTAGCACAGAGAGAGGAAATGGGACCAACACTAGAAATATGCGCCT 11599
QY      541 CCCTTGGTCTGAGAGAGAGAAATCTCTCGTGGTTTCCAGATCTGTACACAGAGATGA 600
Db      11598 CCCTTGGTCTGAGAGAGAGAAATCTCTCGTGGTTTCCAGATCTGTACACAGAGATGA 11539
QY      601 TTCTGAGGGCGGCTGCTGCTGTGGACAATTAAAGGATGAAGTCTGTGAGGGAGTGA 660
Db      11538 TTCTGAGGGCGGCTGCTGCTGTGGACAATTAAAGGATGAAGTCTGTGAGGGAGTGA 11479
QY      661 GGGGAAGACAATCCCTGGAAGACTGATCAGGGGTTCCCTTTGACCCACAGACGCTTGG 720
Db      11478 GGGGAAGACAATCCCTGGAAGACTGATCAGGGGTTCCCTTTGACCCACAGACGCTTGG 11419
QY      721 CACGAGACTTTTCCCTCAGGCGCTTGTCTGCTCCACACTCAATGTGTGGGGGTC 780
Db      11418 CACGAGACTTTTCCCTCAGGCGCTTGTCTGCTCCACACTCAATGTGTGGGGGTC 11359
QY      781 TGACATCCAGCTCTGTGATGCCCTTGGGCGTCCACTCAGGTAGAAAGCGGAGTCCCTCT 840
Db      11358 TGACATCCAGCTCTGTGATGCCCTTGGGCGTCCACTCAGGTAGAAAGCGGAGTCCCTCT 11299
QY      841 CCCCCTCAGAGACTAGAACTTTTCCAAAGAAATAGAGATTATCCAGAGTGGCGGTGCC 900
Db      11298 CCCCCTCAGAGACTAGAACTTTTCCAAAGAAATAGAGATTATCCAGAGTGGCGGTGCC 11239
QY      901 AGGCTGTGTCTGTGGTTCTGTGCTCCCTTCCACCCAGAGTATGTGTTATTATTAGG 960
Db      11238 AGGCTGTGTCTGTGGTTCTGTGCTCCCTTCCACCCAGAGTATGTGTTATTATTAGG 11179
```

```
QY      961 ATGATCATCCAGTGTCTGTGAGTGTCCATGAGAGATGCAAGATGCTTGAATTTTC 1020
Db      11178 ATGATCATCCAGTGTCTGTGAGTGTCCATGAGAGATGCAAGATGCTTGAATTTTC 11119
QY      1021 TGAATCTTCTTTACAGACCCGCCCAAGACACAGGTGACCCACCCCTCTTTGACTAT 1080
Db      11118 TGAATCTTCTTTACAGACCCGCCCAAGACACAGGTGACCCACCCCTCTTTGACTAT 11059
QY      1081 GAGGCCACCTGTAGGTCTGTGGGCGCTTGTACCTGTGCGAGATCATACTGACCTGG 1140
Db      11058 GAGGCCACCTGTAGGTCTGTGGGCGCTTGTACCTGTGCGAGATCATACTGACCTGG 10999
QY      1141 CAGGGGATGGGAGAGACACAGACCCAGAGCTGTGAGACCAAGGCGCTTGACGG 1200
Db      10998 CAGGGGATGGGAGAGACACAGACCCAGAGCTGTGAGACCAAGGCGCTTGACGG 10939
QY      1201 GATGGAACCTTTCAGAAAGTGGGACGTGTGGTGTCTTGTGAGAGAGCAGAGATAC 1260
Db      10938 GATGGAACCTTTCAGAAAGTGGGACGTGTGGTGTCTTGTGAGAGAGCAGAGATAC 10879
QY      1261 ACGTGCATGTGACGATGAGGGGCTGCCGAGCCCTCATGCTGAGATGTGAAGAG 1320
Db      10878 ACGTGCATGTGACGATGAGGGGCTGCCGAGCCCTCATGCTGAGATGTGAAGAG 10819
QY      1321 GGAATGAGGACATCATGTCTGTTAGGAAAGAGAGGCGCTCTGAAAGACCTTTAAG 1380
Db      10818 GGAATGAGGACATCATGTCTGTTAGGAAAGAGAGGCGCTCTGAAAGACCTTTAAG 10759
QY      1381 GGTGCGTGTGAGGGCTGGGGGCTCAGAGACCTTCACCTTCCTTCCAGACAGT 1440
Db      10758 GGTGCGTGTGAGGGCTGGGGGCTCAGAGACCTTCACCTTCCTTCCAGACAGT 10699
QY      1441 CTTCCCTGCGCCACCATCCCATATGGGTATCGTTGCTGGCTGTGTTGCTTGCACGTG 1500
Db      10698 CTTCCCTGCGCCACCATCCCATATGGGTATCGTTGCTGGCTGTGTTGCTTGCACGTG 10639
QY      1501 TAGTCATGTGAGCGTGGGCTGCTGTGTGAGAAAGAGAGCTCAGTAAAGAG 1560
Db      10638 TAGTCATGTGAGCGTGGGCTGCTGTGTGAGAAAGAGAGCTCAGTAAAGAG 10579
QY      1561 GCGTGACAAGTGGGCTGTGAGTTTCTTGTGCCACTGAGGGGTTTCAAGCCCCAGTAGAA 1620
Db      10578 GCGTGACAAGTGGGCTGTGAGTTTCTTGTGCCACTGAGGGGTTTCAAGCCCCAGTAGAA 10519
QY      1621 GTGTGCCCTGCGTGTACTAGGGAAGCAATCCATCCATGATGGGCTTACCAGCGCTGG 1680
Db      10518 GTGTGCCCTGCGTGTACTAGGGAAGCAATCCATCCATGATGGGCTTACCAGCGCTGG 10459
QY      1681 CCCTGTGTGCGAGCACCTTCTTTTGTAAAGCACTGTGACATGAGAGACAGATTTAT 1740
Db      10458 CCCTGTGTGCGAGCACCTTCTTTTGTAAAGCACTGTGACATGAGAGACAGATTTAT 10399
QY      1741 TACCTTATGATTTAGTATGAGGGACCTGATCCAGTAATCAAGGTGAGGAAGGTC 1800
Db      10398 TACCTTATGATTTAGTATGAGGGACCTGATCCAGTAATCAAGGTGAGGAAGGTC 10339
QY      1801 CCTGGCTTAAGACAGACCTTAAGAGGGCACTTGGTGAAGAACCCACATCTGCTTCTTG 1860
Db      10338 CCTGGCTTAAGACAGACCTTAAGAGGGCACTTGGTGAAGAACCCACATCTGCTTCTTG 10279
QY      1861 TTTTTCCTGAT -CGCCCTGGGCTGTGAGTACACATTTTGTGAAACTTTTCAGAGGTC 1918
Db      10278 TTTTTCCTGATCCGCGCTGGGCTGTGAGTACACATTTTGTGAAACTTTTCAGAGGTC 10219
QY      1919 AAGACTAGAGAGTTCCTTAGGACCTCATGGCCCTGCGACCTTTTGGCGCTTCACAGGA 1978
Db      10218 AAGACTAGAGAGTTCCTTAGGACCTCATGGCCCTGCGACCTTTTGGCGCTTCACAGGA 10159
QY      1979 CATTTTCTTCCCAAGATTAAGAAAGAGAGAGAGTCACTCTCAGGCTGCAATAGTATGAA 2038
Db      10158 CATTTTCTTCCCAAGATTAAGAAAGAGAGAGAGTCACTCTCAGGCTGCAATAGTATGAA 10099
```

QY 2039 GGAGGCTGATCCCTGAGATCTTTGGGATCTGTTGGAG-CCATGGGGGAGCTCACC 2097  
|||||  
Db 10098 GGAGGCTGATCCCTGAGATCCTTTGGATCTTGTGTTGGAGCCATGGGGGAGCTCACC 10039  
QY 2098 CACCCACAAATTCCTCTCTGCGCCACATCTCCTGCTCTGACAGGTCGCTTTTG 2157  
|||||  
Db 10038 CACCCACAAATTCCTCTCTGCGCCACATCTCCTGCTCTGACAGGTCGCTTTTG 9979  
QY 2158 TTCTACTCTAGGAGTGAACAGTGGCCAGGGCTCTAATGTCTCTCAGCGCTTGAATG 2217  
|||||  
Db 9978 TTCTACTCTAGGAGTGAACAGTGGCCAGGGCTCTAATGTCTCTCAGCGCTTGAATG 9919  
QY 2218 TGACACCCCGGGGGCCGATGTGTGGGTGTTGAGGGGAAACAGGGGACATAGCTG 2277  
|||||  
Db 9918 TGACACCCCGGGGGCCGATGTGTGGGTGTTGAGGGGAAACAGGGGACATAGCTG 9859  
QY 2278 CTATGAGGTTCTTCTGACTTCATATGATATGACATGTGATGGCGTTTAAAGTGTAC 2337  
|||||  
Db 9858 CTATGAGGTTCTTCTGACTTCATATGATATGACATGTGATGGCGTTTAAAGTGTAC 9799  
QY 2338 CCTGACTGTGACTGATATGATTTTGTTCATGATATTTTCTGTAGTGTGAACAGCTGC 2397  
|||||  
Db 9798 CCTGACTGTGACTGATATGATTTTGTTCATGATATTTTCTGTAGTGTGAACAGCTGC 9739  
QY 2398 CCTGTGTGGACTGAGTGCAAG 2420  
|||||  
Db 9738 CCTGTGTGGACTGAGTGCAAG 9716

RESULT 11  
AF523301 5577 bp DNA linear PRI 03-JUL-2002  
LOCUS Homo sapiens clone WT24 MHC class Ib antigen (HLA-G) gene,  
DEFINITION HLA-G\*01011 allele, complete cds.  
ACCESSION AF523301  
VERSION AF523301.1 GI:21686643  
KEYWORDS human.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5577)  
AUTHORS Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.  
TITLE HLA-E, F, and G polymorphism: genomic sequence defines new  
variation spanning the nonclassical class I genes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 5577)  
AUTHORS Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer  
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA  
98109-1024, USA

FEATURES  
source  
1.3577  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="WT24"  
/gene="HLA-G"  
/allele="HLA-G\*01011"  
join(<1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3766,4123..4127)  
/gene="HLA-G"  
/product="MHC class Ib antigen"  
join(1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3766,4123..4127)  
/gene="HLA-G"  
/codon\_start=1  
/product="MHC class Ib antigen"  
/protein\_id="AA07495.1"  
/db\_xref="GI:21686643"  
/translation="MVVMAPRFLFLLSGLALTLETWAGSHSMRYTSAVSRGRGEP

BASE COUNT 1234 a 1440 c 1533 g 1365 t 5 others  
ORIGIN  
Query Match 98.0%; Score 2393.8; DB 9; Length 5577;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2418; Conservative 0; Mismatches 2; Indels 3; Gaps 2;  
KSSD  
REFAMGVDDTQFEVFNDSASCPMEPRAPWVEQEPYWEETRNKTAHOTDRML  
QTLRGYVNOSEASHTLOMIGCDLGGSGRLRGYQVAYDKDLALNEDRSMTAA  
DTAOLISKRKCPAANVABORAYLEGTGSEKHLRLENGKEMLORADDPKHHTPA  
FDYEATLRCMALGFYPAELILTMORDGDDQDVLYVETRPAGDSTFOKMAVVPSC  
EEORYTCHVQHGSLPEPLMLRKQSSLPFLPMGLVAVGLVLAAYVTAAGAAVLMRK  
KSSD  
QY 1 TACTCCGAGTCTCCGGAGTCTGGGATCCACCCGAGGCGCGGAGCCCGAGACCCCTC 60  
|||||  
Db 1739 TACTCCGAGTCTCCGGAGTCTGGGATCCACCCGAGGCGCGGAGCCCGAGACCCCTC 1798  
QY 61 TACCTGGGAGAACCCCAAGGCGCTTTACCAAAATCCCGCGGGTGGTCCGCGGAGAG 120  
|||||  
Db 1799 TACCTGGGAGAACCCCAAGGCGCTTTACCAAAATCCCGCGGGTGGTCCGCGGAGAG 1858  
QY 121 CGAGGCTGGTGGGGGGGCTGACCGAGGGGTGGGGGCTTCTACACCTCCAGTG 180  
|||||  
Db 1859 CGAGGCTGGTGGGGGGGCTGACCGAGGGGTGGGGGCTTCTACACCTCCAGTG 1918  
QY 181 GATGATGGCTGCGACTGGGGTCCGACGAGCGCTCTCCGCGGGTATGACAGATATGC 240  
|||||  
Db 1919 GATGATGGCTGCGACTGGGGTCCGACGAGCGCTCTCCGCGGGTATGACAGATATGC 1978  
QY 241 CTACGATGCGAAGATTTACCTCGCCCTTACAGAGAGACTCGGCTCTGAGCCGAGCGA 300  
|||||  
Db 1979 CTACGATGCGAAGATTTACCTCGCCCTTACAGAGAGACTCGGCTCTGAGCCGAGCGA 2038  
QY 301 CACTCGGCTCAGATCTCCAAAGCGCAAGTGTAGGCGGGCCCAATGTGGTGAACAAAGAG 360  
|||||  
Db 2039 CACTCGGCTCAGATCTCCAAAGCGCAAGTGTAGGCGGGCCCAATGTGGTGAACAAAGAG 2098  
QY 361 AGCTTACCTGAGGCGACGTGCTGAGTGTGCTCCACAGATACCTGAGAACGGAAGA 420  
|||||  
Db 2099 AGCTTACCTGAGGCGACGTGCTGAGTGTGCTCCACAGATACCTGAGAACGGAAGA 2158  
QY 421 GATCTGCGAGCGCGGGGTACCAAGGGGCGAGTGGGGCGCTCTGTATGAGACT 480  
|||||  
Db 2159 GATCTGCGAGCGCGGGGTACCAAGGGGCGAGTGGGGCGCTCTGTATGAGACT 2218  
QY 481 CTCAGCCTGGCTGACCAAGAGAGAGGAAATGGGACCAACACTAGATATATGCGCT 540  
|||||  
Db 2219 CTCAGCCTGGCTGACCAAGAGAGAGGAAATGGGACCAACACTAGATATATGCGCT 2278  
QY 541 CCTCTGGTCTGAGGAGAGAAATCCCTGCGGTTTCCAGATCTGTACAGAGAGTGA 600  
|||||  
Db 2279 CCTCTGGTCTGAGGAGAGAAATCCCTGCGGTTTCCAGATCTGTACAGAGAGTGA 2338  
QY 601 TTCTGAGGGCGCCGCTGCTCTGTGGGACAAATTAAGGATCAAGTCTGTGAGGAGTGA 660  
|||||  
Db 2339 TTCTGAGGGCGCCGCTGCTCTGTGGGACAAATTAAGGATCAAGTCTGTGAGGAGTGA 2398  
QY 661 GGGGAAGACAATCCCTGGAAGACATGATCAGGGGTTCCTTGGACCCACAGCAGCTTGG 720  
|||||  
Db 2399 GGGGAAGACAATCCCTGGAAGACATGATCAGGGGTTCCTTGGACCCACAGCAGCTTGG 2458  
QY 721 CACGAGACTTTTCCCTCAGGCGCTTGTCTGCTCAGACTCAATGTGTGAGGGGTC 780  
|||||  
Db 2459 CACGAGACTTTTCCCTCAGGCGCTTGTCTGCTCAGACTCAATGTGTGAGGGGTC 2518  
QY 781 TGACTCAGCTCTCTGATGTCCTTGGGCTTCACACTAGGTGAGAACCGGAGGTCTGCT 840  
|||||  
Db 2519 TGACTCAGCTCTCTGATGTCCTTGGGCTTCACACTAGGTGAGAACCGGAGGTCTGCT 2578  
QY 841 CCCCCTCAGAGACTGAGCTTTCCAAAGGATAGAGATTAATCCAGGTGCCCTGTCC 900  
|||||  
Db 2579 CCCCCTCAGAGACTGAGCTTTCCAAAGGATAGAGATTAATCCAGGTGCCCTGTCC 2638



QY 901 AGCGTGTGTCGTGCTCTGTCGTCCTTCCGCCAGACCAGATATCGTTTCATTTAGG 960  
|||||  
Db 2639 AGCGTGTGTCGTGCTCTGTCGTCCTTCCGCCAGACCAGATATCGTTTCATTTAGG 2698  
QY 961 ATGTGTCAATCCAGAGTCTGCTGAGTGTCCCATAGAGATGCAAAAGTCTTGAATTTTC 1020  
|||||  
Db 2699 ATGTGTCAATCCAGAGTCTGCTGAGTGTCCCATAGAGATGCAAAAGTCTTGAATTTTC 2758  
QY 1021 TGACTCTTCCCTTTAGACCCCCCAAGACACAGTGCACACACCTGTCTTGACTAT 1080  
|||||  
Db 2759 TGACTCTTCCCTTTAGACCCCCCAAGACACAGTGCACACACCTGTCTTGACTAT 2818  
QY 1081 GAGCCACACCCCTGAGTGTGAGCCCTGAGGCTTACCCCTGGAGATCATACTAGCTGG 1140  
|||||  
Db 2819 GAGCCACACCCCTGAGTGTGAGCCCTGAGGCTTACCCCTGGAGATCATACTAGCTGG 2878  
QY 1141 CAGCGGATGAGGAGAGACACAGACCAGAGCTGTGAGACAGGCTGCAGGG 1200  
|||||  
Db 2879 CAGCGGATGAGGAGAGACACAGACCAGAGCTGTGAGACAGGCTGCAGGG 2938  
QY 1201 GATGGAACCTTCCAGAACTGGGCGAGCTGTGTGCTTGTGAGAGAGACAGATAC 1260  
|||||  
Db 2939 GATGGAACCTTCCAGAACTGGGCGAGCTGTGTGCTTGTGAGAGAGACAGATAC 2998  
QY 1261 ACGTGCCATGTGACAGCATGAGGGGCTGCCGAGCCCTCATGCTGAGATGAGTAAGATAC 1320  
|||||  
Db 2999 ACGTGCCATGTGACAGCATGAGGGGCTGCCGAGCCCTCATGCTGAGATGAGTAAGATAC 3058  
QY 1321 GGAGATGAGGACATCATGTCTGTTAGGGAAGACAGAGCCCTCTGAAAGACCTTTAACAG 1380  
|||||  
Db 3059 GGAGATGAGGACATCATGTCTGTTAGGGAAGACAGAGCCCTCTGAAAGACCTTTAACAG 3118  
QY 1381 GGTGCGTGTGAGGGCTGTGGGGGTGAGAGACCCCTGACCTTCACCTCTTCCACAGACAGT 1440  
|||||  
Db 3119 GGTGCGTGTGAGGGCTGTGGGGGTGAGAGACCCCTGACCTTCACCTCTTCCACAGACAGT 3178  
QY 1441 CTTCCCTCCACCATCTCCCATCATGAGGTATGCTGTGCGCTGAGTTGCTTCCAGAGTGC 1500  
|||||  
Db 3179 CTTCCCTCCACCATCTCCCATCATGAGGTATGCTGTGCGCTGAGTTGCTTCCAGAGTGC 3238  
QY 1501 TAGTCATGAGAGCTGCGGTGCTGCTGTGTGTGTGAGAAAGAAAGAGCTCAGGTAAAGAG 1560  
|||||  
Db 3239 TAGTCATGAGAGCTGCGGTGCTGCTGTGTGTGTGAGAAAGAAAGAGCTCAGGTAAAGAG 3298  
QY 1561 GGGTACAAAGTGGGGTGTGAGTTTCTGTGCCACTGTGGGGTTTCAACCCCAAGGTAAAG 1620  
|||||  
Db 3299 GGGTACAAAGTGGGGTGTGAGTTTCTGTGCCACTGTGGGGTTTCAACCCCAAGGTAAAG 3358  
QY 1621 GTGTGCCCTGCTGTGTTACTGTGGAAGACATCCACACTCATGTGGGCTTACCCAGGCTGGG 1680  
|||||  
Db 3359 GTGTGCCCTGCTGTGTTACTGTGGAAGACATCCACACTCATGTGGGCTTACCCAGGCTGGG 3418  
QY 1681 CCTGTGTGCCAGACCTTCTCTTTTGTAAAGACCTGTGACATATGAAGACAGATTTAT 1740  
|||||  
Db 3419 CCTGTGTGCCAGACCTTCTCTTTTGTAAAGACCTGTGACATATGAAGACAGATTTAT 3478  
QY 1741 TACCTTGATGATTTAGTATGATGGGAGCCGATCCAGTAATCACAGGTGAGGAAGGTC 1800  
|||||  
Db 3479 TACCTTGATGATTTAGTATGATGGGAGCCGATCCAGTAATCACAGGTGAGGAAGGTC 3538  
QY 1801 CCTGTGTAAGACACACCTTAAAGAGGAGATTGTGTGAGAGCCACATCTGCTTCTCTG 1860  
|||||  
Db 3539 CCTGTGTAAGACACACCTTAAAGAGGAGATTGTGTGAGAGCCACATCTGCTTCTCTG 3598  
QY 1861 TTTTTCCTGAT--CGCCCTGGGTGTGCACTACACATTTCTGGAACCTTCTGAGGGTCC 1918  
|||||  
Db 3599 TTTTTCCTGATCCCGCCCTGGGTGTGCACTACACATTTCTGGAACCTTCTGAGGGTCC 3658  
QY 1919 AAGACTAGGAGGTCTCTAGGACCTCATGGCCCTGACCTTCTGGGCTCTCACAGGA 1978  
|||||  
Db 3659 AAGACTAGGAGGTCTCTCTAGGACCTCATGGCCCTGACCTTCTGGGCTCTCACAGGA 3718  
QY 1979 CATTTTCTTCCACAGATTGAAGAGGAGAGCTACTCTCAGGCTGCAAGTAAGTATGAA 2038

Db 3719 CATTTTCTTCCACAGATTGAAGAGGAGAGCTACTCTCAGGCTGCAAGTAAGTATGAA 3778  
QY 2039 GGAAGCTGATCCCTGAGATTCCTTGGGATCTTGTGTTGGGAG-CCATGGGGAGACTCAC 2097  
|||||  
Db 3779 GGAAGCTGATCCCTGAGATTCCTTGGGATCTTGTGTTGGGAGCCATGGGGAGGCTCAC 3838  
QY 2098 CACCCACAAATTCCTCTCGGGCACATCTCCGTGAGTCTGACAGAGTGTGTTTTTG 2157  
|||||  
Db 3839 CACCCACAAATTCCTCTCTGAGATTCCTGAGATTCCTGAGTGTGAGTGTGTTTTTG 3898  
QY 2158 TTCTACTTAAAGCAGTACAGTGTCCAGAGGCTCTAATGTCTCTACAGGCTTGAATG 2217  
|||||  
Db 3899 TTCTACTTAAAGCAGTACAGTGTCCAGAGGCTCTAATGTCTCTACAGGCTTGAATG 3958  
QY 2218 TGACACCCCGGGGGGCTGATGTGTGGGTGTTTAAAGGAACAGGAGACATAGCTGTG 2277  
|||||  
Db 3959 TGACACCCCGGGGGGCTGATGTGTGGGTGTTTAAAGGAACAGGAGACATAGCTGTG 4018  
QY 2278 CTATGAGTTCTTTTACCTCATATGATTAGAGCATGTGATGGGCTGTTTAAAGTGTAC 2337  
|||||  
Db 4019 CTATGAGTTCTTTTACCTCATATGATTAGAGCATGTGATGGGCTGTTTAAAGTGTAC 4078  
QY 2338 CTTCACTGTGACATGATATGAAATTTTTCATGAATATTTTCTGTAGTGTGAACAGCTGC 2397  
|||||  
Db 4079 CTTCACTGTGACATGATATGAAATTTTTCATGAATATTTTCTGTAGTGTGAACAGCTGC 4138  
QY 2398 CTTGTGTGGAGCATGATGGGCAAG 2420  
|||||  
Db 4139 CTTGTGTGGAGCATGATGGGCAAG 4161  
RESULT 12  
AF523302 5577 bp DNA linear PRI 03-JUL-2002  
LOCUS  
DEFINITION Homo sapiens clone MDV MHC class Ib antigen (HLA-G) gene,  
AF523302  
ACCESSION  
VERSION AF523302  
KEYWORDS AF523302.1 GI:21686645  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5577)  
Ishitani,A., Miki,A., Williams,L.M., Moore,Y., and Geraghty,D.E.  
HLA-E, F, and G polymorphism: genomic sequence defines new  
variation spanning the nonclassical class I genes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 5577)  
Ishitani,A., Miki,A., Williams,L.M., Moore,Y., and Geraghty,D.E.  
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA  
TITLE Direct Submission  
JOURNAL Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer  
Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA  
98109-1024, USA  
FEATURES  
source location/Qualifiers  
1..5577  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="MDV"  
/gene="HLA-G"  
/allele="HLA-G\*01011"  
/join(<1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3766,4123..4127)  
/gene="HLA-G"  
/product="MHC class Ib antigen"  
/join(1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3739)  
/gene="HLA-G"  
/codon\_start=1  
/product="MHC class Ib antigen"

```

/protein_id="AAW74996.1"
/db_xref="GI:21686646"
/translation="MVVMAPRTLLFLLSGALTLLETWAGSHSKRYEFAAASVRGPEP
RFIAMGYDDTOFVRDSDSCPRMEPRRAVWDEGEVEEETRMKAAQIDRNL
OTLRGYNOSEASSHLDMWICGLDSDGLLGYBDYATDGDYIALNEDLSMTAA
DTAAQISKRKCEAANVAEORATLEGTCCVLMIRYLENGEMQIRADPPTHTHPV
FDVEATIRCMALPEYPAEILLITWQRODEBDTQDVEYTERPADGTFQKMAAVVPSG
EQRRTYCHVHDEGLPEPLMLRMKQSSIPITPIGIVAGLVLAAYVTAAYVLMRK
KSSSD"
BASE COUNT      1234 a      1440 c      1533 g      1365 t      5 others
ORIGIN
Query Match      98.0%; Score 2393.8; DB 9; Length 5577;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2418; Conservative 0; Mismatches 2; Indels 3; Gaps 2;
QY 1 TACGCCAGTCTCCGGGTCGGGATCCACCCGAGGGCCGGGAGACCCGCCAGACCTC 60
Db 1739 TACTCCCGAGTCTCCGGGTCTGGGATCCACCCGAGGGCCGGGAGACCCCTC 1798
QY 61 TACCTGGAGAACCCCAAGGCGCTTTACCAAAATCCCGGGGTGGTCCGGGCGAGG 120
Db 1799 TACCTGGAGAACCCCAAGGCGCTTTACCAAAATCCCGGGGTGGTCCGGGCGAGG 1858
QY 121 CGAGGCTCGGTGGGGCGGCGTCAACCGAGGGGTGGGCCAGTTCTCAACCCCTCAGT 180
Db 1859 CGAGGCTCGGTGGGGCGGCGTCAACCGAGGGGTGGGCCAGTTCTCAACCCCTCAGT 1918
QY 181 GATGATTGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGGGGGTATGAAAGATATG 240
Db 1919 GATGATTGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGGGGGTATGAAAGATATG 1978
QY 241 CTACGATGCGAAGGATTACCTCGCCCTGAACGAGACCTGCGCTCTGACCCGACGGA 300
Db 1979 CTACGATGCGAAGGATTACCTCGCCCTGAACGAGACCTGCGCTCTGACCCGACGGA 2038
QY 301 CACGCGGCGTCAGATCTCCCAAGGCGCAAGTGTAGGGGGCCAAATGTGCTGAACAAAGAG 360
Db 2039 CACGCGGCGTCAGATCTCCCAAGGCGCAAGTGTAGGGGGCCAAATGTGCTGAACAAAGAG 2098
QY 361 AGCCTACCTGAGAGGACGTCGCTGAGTGGCTCCACAGATACCTGAGAGAGGGAAGA 420
Db 2099 AGCCTACCTGAGAGGACGTCGCTGAGTGGCTCCACAGATACCTGAGAGAGGGAAGA 2158
QY 421 GATGCTGCAACGCGCGGGGTACCAAGGGCACTGGGGCGCTCCCTGATCTCTGTAGACCT 480
Db 2159 GATGCTGCAACGCGCGGGGTACCAAGGGCACTGGGGCGCTCCCTGATCTCTGTAGACCT 2218
QY 481 CTGAGCCTGCTAGACCAAGAGAGAGAGAAATGGAGAACCAACATAGAAATATGCGCCT 540
Db 2219 CTGAGCCTGCTAGACCAAGAGAGAGAGAAATGGAGAACCAACATAGAAATATGCGCCT 2278
QY 541 CCTCTGTGCTTGAAGGAGAGAAATCTCTGTGGTTTCCAGATCTCTGACAGAGAGTGA 600
Db 2279 CCTCTGTGCTTGAAGGAGAGAAATCTCTGTGGTTTCCAGATCTCTGACAGAGAGTGA 2338
QY 601 TTCTGAGGGCCCTCTCTGCTCTCTGAGACAATTAAGGATGAAGTCTCTGAGGAGTGA 660
Db 2339 TTCTGAGGGCCCTCTCTGCTCTCTGAGACAATTAAGGATGAAGTCTCTGAGGAGTGA 2398
QY 661 GGGGAGACAAATCCCTGGAAGACTGATCAGGGGTTCCCTTTAGACCCCAAGAGAGCTTGG 720
Db 2399 GGGGAGACAAATCCCTGGAAGACTGATCAGGGGTTCCCTTTAGACCCCAAGAGAGCTTGG 2458
QY 721 CACCAAGACTTTTCCCTCAGGACTTGTCTCTGCTCACAATCATATGATGTGGGGGTC 780
Db 2459 CACCAAGACTTTTCCCTCAGGACTTGTCTCTGCTCACAATCATATGATGTGGGGGTC 2518
QY 781 TGACTCCACTCTCTGAGTCCCTTGGCTCCACTCAGTCAAGACGAGAGTCCCTGCT 840
Db 2519 TGACTCCACTCTCTGAGTCCCTTGGCTCCACTCAGTCAAGACGAGAGTCCCTGCT 2578
QY 841 CCCCGCTCAGAGACTAGAACTTTCCAAAGGATAGAGATTATCCAGAGTGGCCGTGTC 900

```

```

|||||
Db 2579 CCCCCCTCAGACACTAGAACTTTCCAAAGATAGAGATTATCCAGAGTGGCCGTGTC 2638
QY 901 AGCCTGTGTGTGGTCTGTGTCTCCCTTCCACCCAGATGTGTCTTCTTCTTGTAG 960
Db 2639 AGCCTGTGTGTGGTCTGTGTCTCCCTTCCACCCAGATGTGTGTCTTCTTGTAG 2698
QY 961 ATGCTACATCCAGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 2699 ATGCTACATCCAGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2758
QY 1021 TGACTCTTCTTTCAACACCCCCCAAGACACACAGTACACCCACCTGTCTTGTACTAT 1080
Db 2759 TGACTCTTCTTTCAACACCCCCCAAGACACACAGTACACCCACCTGTCTTGTACTAT 2818
QY 1081 GAGCCACCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
Db 2819 GAGCCACCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2878
QY 1141 CAGCGGATGGGGAGGACCAAGACCAAGAGACGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
Db 2879 CAGCGGATGGGGAGGACCAAGACCAAGAGACGTGTGTGTGTGTGTGTGTGTGTGTGT 2938
QY 1201 GATGAACCTTCCAGAAAGTGGGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db 2939 GATGAACCTTCCAGAAAGTGGGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2998
QY 1261 ACCTGCATGTGTACACATGAGGGGCTGCCGGAACCCCTCATGTGTGTGTGTGTGTGT 1320
Db 2999 ACCTGCATGTGTACACATGAGGGGCTGCCGGAACCCCTCATGTGTGTGTGTGTGTGT 3058
QY 1321 GGAGATGGAGGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Db 3059 GGAGATGGAGGATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3118
QY 1381 GGTGCGGTGTAGGGGCTGGGGGTGAGAGACCTCAGCTTCACTCTCTTCCAGAGCAGT 1440
Db 3119 GGTGCGGTGTAGGGGCTGGGGGTGAGAGACCTCAGCTTCACTCTCTTCCAGAGCAGT 3178
QY 1441 CTTCCTCCCAACCATCCCAATCATGGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Db 3179 CTTCCTCCCAACCATCCCAATCATGGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3238
QY 1501 TAGTACTGAGAGCTGCGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
Db 3239 TAGTACTGAGAGCTGCGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3298
QY 1561 GGGTGACAAGTGGGCTGTGATTTTCTTGTCCCACTGGGGGTTTCAAGCCCCAGGTGAA 1620
Db 3299 GGGTGACAAGTGGGCTGTGATTTTCTTGTCCCACTGGGGGTTTCAAGCCCCAGGTGAA 3358
QY 1621 GTGTGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Db 3359 GTGTGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3418
QY 1681 CCTGTGTGCCAGCACCTTCTCTTTGTAAAGCACCTGTGACATGATGAAGACAGATTAT 1740
Db 3419 CCTGTGTGCCAGCACCTTCTCTTTGTAAAGCACCTGTGACATGATGAAGACAGATTAT 3478
QY 1741 TACCTTGTATTTAGTATGAGGAGCTGATCCAGATTAATCAAGGTCAAGGAAAGTTC 1800
Db 3479 TACCTTGTATTTAGTATGAGGAGCTGATCCAGATTAATCAAGGTCAAGGAAAGTTC 3538
QY 1801 CCTGGCTAAGGACAGACCTTAAGAGGGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
Db 3539 CCTGGCTAAGGACAGACCTTAAGAGGGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3598
QY 1861 TTTTCTCTGAT - CGCCCTGGGCTGTGAGTCAACATTTTGTGAAACTTGTGAGGGTTC 1918
Db 3599 TTTTCTCTGATCCCGGCTGTGGGTGTGAGTCAACATTTTGTGAAACTTGTGAGGGTTC 3658
QY 1919 AAGACTGAGAGGTTCTGTGAGACTCATGTGCTGACCTTGTGCTGTGACAGGA 1978

```

Db	3659	AAGACTAGAGAGTTCCTCTAGACCTCATGACCCTTGCCACCTTCTGAGCTCTGCACAGA	3718
Qy	1979	CATTTCCTCCACAGATGTAAGAAGAGGAGCGTACTCTCAGGCTGCAGTAAGTATGAA	2038
Db	3719	CATTTCCTCCACAGATGTAAGAAGAGGAGGACTACTCTCAGGCTGCAGTAAGTATGAA	3778
Qy	2039	GGAGGCTGATCCCTGAGATCTTGGGATCTTGTGGGAG-CCATGGGGAGACTCACC	2097
Db	3779	GGAGGCTGATCCCTGAGATCTTGGGATCTTGTGGGAGGCCCATGGGGAGACTCACC	3838
Qy	2098	CACCCCAATTCCTCTCTGGCCACATCTCTGTGCTCTCTGACAGAGTCTGTTTTTG	2157
Db	3839	CACCCCAATTCCTCTCTGGCCACATCTCTGTGCTCTCTGACAGAGTCTGTTTTTG	3898
Qy	2158	TTCTACTCTAGGAGTGCAGTGCCTGACGAGGCTCAATGCTCTCTCAGGCTTGAATG	2217
Db	3899	TTCTACTCTAGGAGTGCAGTGCCTGACGAGGCTCAATGCTCTCTCAGGCTTGAATG	3958
Qy	2218	TGACACCCCGGGGGCCGATGTGTGGGTTGTTGAGGGGACAGGAGCATAGCTGTG	2277
Db	3959	TGACACCCCGGGGGCCGATGTGTGGGTTGTTGAGGGGACAGGAGCATAGCTGTG	4018
Qy	2278	CTATGAGGTTTCTTTGACTTCATGATGATGAGCATGTGATGGCTGTTTAAAGTGCACC	2337
Db	4019	CTATGAGGTTTCTTTGACTTCATGATGATGAGCATGTGATGGCTGTTTAAAGTGCACC	4078
Qy	2338	CCTCAGCTGTGACTGATGATTTTGTTCATGATATTTTCTGTAGTGTGAAGAGCTGC	2397
Db	4079	CCTCAGCTGTGACTGATGATTTTGTTCATGATATTTTCTGTAGTGTGAAGAGAGTGC	4138
Qy	2398	CCTGTGTGGAGCTGATGGCAAG 2420	
Db	4139	CCTGTGTGGAGCTGATGGCAAG 4161	
RESULT 13	AF523298	5574 bp DNA linear PRI 03-JUL-2002	
LOCUS	AF523298	Homo sapiens clone SCHU MHC class Ib antigen (HLA-G) gene,	
DEFINITION	AF523298	HLA-G*0101 allele, complete cds.	
ACCESSION	AF523298.1	GI:21686638	
VERSION			
KEYWORDS			
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 5574)	
JOURNAL		Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.	
REFERENCE		HLA-E, F, and G polymorphism: genomic sequence defines new	
AUTHORS		variation spanning the nonclassical class I genes	
TITLE		Unpublished	
JOURNAL		2 (bases 1 to 5574)	
REFERENCE		Ishihara, A., Miki, A., Williams, L.M., Moore, Y., and Geraghty, D.E.	
AUTHORS		Direct Submission	
TITLE		Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer	
JOURNAL		Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA	
FEATURES		98109-1024, USA	
SOURCE		Location/Qualifiers	
		1..5574	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/chromosome="6"	
		/clone="SCHU"	
		<1202..>4127	
		/gene="HLA-G"	
		/allele="HLA-G*0101"	
		join(<1202..1274,1404..1673,1900..2175,2775..3050,	
		3173..3289,3735..3766,4123..>4127)	
		/gene="HLA-G"	
		/product="MHC class Ib antigen"	
		join(1202..1274,1404..1673,1900..2175,2775..3050,	
		3173..3289,3735..3739)	

Qy	1	TACTCCGAGTTCCTCGGCTGTGGATTCACCCGAGGCGCGGAGCCCGGAGACCTTC	60
Db	1739	TACTCCGAGTTCCTCGGCTGTGGATTCACCCGAGGCGCGGAGCCCGGAGACCTTC	1798
Qy	61	TACTGGGAGAACCCCAAGGCGCTTTACCAAAATCCCGGGGTGGTCCGGGCGAGGG	120
Db	1799	TACTGGGAGAACCCCAAGGCGCTTTACCAAAATCCCGGGGTGGTCCGGGCGAGGG	1858
Qy	121	CGAGGCTCGGTGGGCGGCGGTGACCGAGGGGGTGGGGCCAGTTCTCACACCTCCAGTG	180
Db	1859	CGAGGCTCGGTGGGCGGCGGTGACCGAGGGGGTGGGGCCAGTTCTCACACCTCCAGTG	1918
Qy	181	GATGATTTGGCTGGGAGCTGGGGTCCGAGGAGCGCTCTCCGGGGATGAACAGATATGC	240
Db	1919	GATGATTTGGCTGGGAGCTGGGGTCCGAGGAGCGCTCTCCGGGGATGAACAGATATGC	1978
Qy	241	CTACGATGGCAAGATTATCTCCCTGAACGAGAGCTGCGCTCTGACCCGACCGGA	300
Db	1979	CTACGATGGCAAGATTATCTCCCTGAACGAGAGCTGCGCTCTGACCCGACCGGA	2038
Qy	301	CATCGCGGCTCATATCTCCAAAGGCGCAAGTGTGAGGGGCGCAATGTGGTGAACAAAGAG	360
Db	2039	CATCGCGGCTCATATCTCCAAAGGCGCAAGTGTGAGGGGCGCAATGTGGTGAACAAAGAG	2098
Qy	361	AGCTTACCTGAGGAGGACGTGCGTGTGAGTGGCTCCACAGATACCTGTAGAGAGGA	420
Db	2099	AGCTTACCTGAGGAGGACGTGCGTGTGAGTGGCTCCACAGATACCTGTAGAGAGGA	2158
Qy	421	GATGCTGACGCGCGGGGTACCAAGGGGCACTGGGGCGCTCCCTGATCTCTAGACCT	480
Db	2159	GATGCTGACGCGCGGGGTACCAAGGGGCACTGGGGCGCTCCCTGATCTCTAGACCT	2218
Qy	481	CTCAGCGCTGGGCTTACCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	540
Db	2219	CTCAGCGCTGGGCTTACCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2278
Qy	541	CCCTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	600
Db	2279	CCCTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2338
Qy	601	TTCTGAGGCGCGTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
Db	2339	TTCTGAGGCGCGTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2398
Qy	661	GGGGAAGACAAATCCCTGGAAGACATGATGAGGGGTCCCTTGAACCCACAGAGGCTTGG	720
Db	2399	GGGGAAGACAAATCCCTGGAAGACATGATGAGGGGTCCCTTGAACCCACAGAGGCTTGG	2458
Qy	721	CACGAGACTTTTCCCTCAGGCGCTTCTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGG	780
Db	2459	CACGAGACTTTTCCCTCAGGCGCTTCTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGG	2518
Qy	781	TGACTCCAGCTCTCTGAGTCCCTTGGCTTCACATGATGATGATGATGATGATGATGATGATG	840

Db 2519 TGACTCCAGCTCTCTGTAGTCCCTTGGCTTCACCTCAGGTGAGAACCGAGGTCCTCT 2578  
QY 841 CCCCCGCTCAGAGACTAGAACTTTCAGAAAGATAGAGATTATCCAGGTGCGGTGCC 900  
Db 2579 CCCCCGCTCAGAGACTAGAACTTTCAGAAAGATAGAGATTATCCAGGTGCGGTGCC 2638  
QY 901 AGGCTGTCTGTGGTCTGTGCTCCCTTCCACCCAGGTATCTGGTTCATTCTTAGG 960  
Db 2639 AGGCTGTCTGTGGTCTGTGCTCCCTTCCACCCAGGTATCTGGTTCATTCTTAGG 2638  
QY 961 ATGGTCACATCCAGGTCTGTGTGAGTGTCCATGAGAGATGCAAAAGCTTGAATTTTC 1020  
Db 2699 ATGGTCACATCCAGGTCTGTGTGAGTGTCCATGAGAGATGCAAAAGCTTGAATTTTC 2758  
QY 1021 TGACTCTCTCTGTAGAGACCCCAAGACACAGCTGACCCACACCTGTCTTTAGCAT 1080  
Db 2759 TGACTCTCTCTGTAGAGACCCCAAGACACAGCTGACCCACACCTGTCTTTAGCAT 2818  
QY 1081 GAGGCCACCTGAGGTCTGTGGGCTTCCACCTGGGAGATCATAGACTGG 1140  
Db 2819 GAGGCCACCTGAGGTCTGTGGGCTTCCACCTGGGAGATCATAGACTGG 2878  
QY 1141 CAGCGGATGGGGAGACCAAGACAGAGAGTGGAGTCTGTGAGACAGGCTTGCAGGG 1200  
Db 2879 CAGCGGATGGGGAGACCAAGACAGAGAGTGGAGTCTGTGAGACAGGCTTGCAGGG 2938  
QY 1201 GATGCAACCTTCAGAAAGTGGGAGCTGTGTGTGCTTCTGTGAGAGAGAGATATAC 1260  
Db 2939 GATGCAACCTTCAGAAAGTGGGAGCTGTGTGTGCTTCTGTGAGAGAGAGATATAC 2998  
QY 1261 ACCTGCCATGTGAGCATGAGGGGCTGCCGAGCCCTCATGTCTGAGATGGAGTAGAG 1320  
Db 2999 ACCTGCCATGTGAGCATGAGGGGCTGCCGAGCCCTCATGTCTGAGATGGAGTAGAG 3058  
QY 1321 GGAGATGAGGACATCATGTCTGTAGGAAAGAGAGGCTCTGTGAAGACCTTTAACAG 1380  
Db 3059 GGAGATGAGGACATCATGTCTGTAGGAAAGAGAGGCTCTGTGAAGACCTTTAACAG 3118  
QY 1381 GATCGGTGTGAGGGGTGGGGGTCCAGAGACCTCACCTTCACCTTCCAGAGAGT 1440  
Db 3119 GATCGGTGTGAGGGGTGGGGGTCCAGAGACCTCACCTTCACCTTCCAGAGAGT 3178  
QY 1441 CTTCCTGCCCCACCATCCCATCATGAGGTATGCTTGTGCTGCTGCTTGTCTTGCACGTG 1500  
Db 3179 CTTCCTGCCCCACCATCCCATCATGAGGTATGCTTGTGCTGCTGCTTGTCTTGCACGTG 3238  
QY 1501 TAGTCACTGAGTGTGCGTGTGCTGTGTGGAGAAAGAGAGTCCAGTAAAGAG 1560  
Db 3239 TAGTCACTGAGTGTGCGTGTGCTGTGTGGAGAAAGAGAGTCCAGTAAAGAG 3298  
QY 1561 GGGTGAACAAGTGGGTCTGAGTTTCTGTCCACTGGGGGTTTCAAGCCCCAGTAGAA 1620  
Db 3299 GGGTGAACAAGTGGGTCTGAGTTTCTGTCCACTGGGGGTTTCAAGCCCCAGTAGAA 3358  
QY 1621 GGTGTGCGCGGTGTACTGGGAACACACATCATATGAGGCTTACCCAGCTGGG 1680  
Db 3359 GGTGTGCGCGGTGTACTGGGAACACACATCATATGAGGCTTACCCAGCTGGG 3418  
QY 1681 CCCTGTGTGCGACACCTTCTCTTTTGAAGACCTGTGACATGAAAGACAGATTAT 1740  
Db 3419 CCCTGTGTGCGACACCTTCTCTTTTGAAGACCTGTGACATGAAAGACAGATTAT 3478  
QY 1741 TACCTTGATGATTGATGATGAGGACCTGATCCAGTATATCAGAGTCAAGAGAGTTC 1800  
Db 3479 TACCTTGATGATTGATGATGAGGACCTGATCCAGTATATCAGAGTCAAGAGAGTTC 3538  
QY 1801 CCGGTGTAAGGACAGACCTTAGAGAGGAGTGTGTGAGAGACCCACATCTGCTTCTTGG 1860  
Db 3539 CCGGTGTAAGGACAGACCTTAGAGAGGAGTGTGTGAGAGACCCACATCTGCTTCTTGG 3598  
QY 1861 TTTTTCCTGAT--CGCCCTGGGTCTGACATGACACATTTCTGGAACCTCTGAGGGTCC 1918  
Db 3599 TTTTTCCTGATCCCGCCCTGGGTCTGACATGACACATTTCTGGAACCTCTGAGGGTCC 3658

QY 1919 AAGACTAGAGGTTCTCTAGAGCTCATGGCCCTGACCTTTCTGTGCTTCACAGGA 1978  
Db 3659 AAGACTAGAGGTTCTCTAGAGCTCATGGCCCTGACCTTTCTGTGCTTCACAGGA 3718  
QY 1979 CATTTTCTCCACAGATTGAAAGAGAGAGCTACTCTCAGGGCGCAAGTAAGTAGAA 2038  
Db 3719 CATTTTCTCCACAGATTGAAAGAGAGAGCTACTCTCAGGGCGCAAGTAAGTAGAA 3778  
QY 2039 GGAGGCTGATCCCTGAGATCCCTTGGATCTGTGTGGAG-CCATGGGGAGCTCAC 2097  
Db 3779 GGAGGCTGATCCCTGAGATCCCTTGGATCTGTGTGGAGCCCATGGGGAGCTCAC 3838  
QY 2098 CAGCCCAATTTCTCTCTGGCCACATCTCTGTGCTGTGACAGGTCTGTTTTG 2157  
Db 3839 CAGCCCAATTTCTCTCTGGCCACATCTCTGTGCTGTGACAGGTCTGTTTTG 3898  
QY 2158 TTCTACTGTAGGAGTACAGTCCAGGGCTTAATGTCTCTACAGGCTTGAATG 2217  
Db 3899 TTCTACTGTAGGAGTACAGTCCAGGGCTTAATGTCTCTACAGGCTTGAATG 3958  
QY 2218 TGACACCCCGGGGCGCTGATGTGTGGTTGTTGAGGGAGACAGGACATAGCTGTG 2277  
Db 3959 TGACACCCCGGGGCGCTGATGTGTGGTTGTTGAGGGAGACAGGACATAGCTGTG 4018  
QY 2278 CTATGAGGTTTCTTGAATGATATGAGCATGTGATGGGTCTTTAAAGTGTACC 2337  
Db 4019 CTATGAGGTTTCTTGAATGATATGAGCATGTGATGGGTCTTTAAAGTGTACC 4078  
QY 2338 CCTCACTGTAGCATGATATGATTTGTTCAATGATATTTTCTGTAGTGAACAGCTGC 2397  
Db 4079 CCTCACTGTAGCATGATATGATTTGTTCAATGATATTTTCTGTAGTGAACAGCTGC 4138  
QY 2398 CTTGTGTGGACTGATGGCAAG 2420  
Db 4139 CTTGTGTGGACTGATGGCAAG 4161

RESULT 14  
AF523305 5574 bp DNA linear PRI 03-JUL-2002  
LOCUS AF523305  
DEFINITION Homo sapiens clone HOM2 MHC class Ib antigen (HLA-G) gene,  
HLA-G\*01011 allele, complete cds.  
ACCESSION AF523305  
VERSION AF523305.1 GI:21686651  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 5574)  
AUTHORS Ishihara, A., Miki, A., Williams, L.M., Moore, Y. and Geraghty, D.E.  
TITLE HLA-E, F, and G polymorphism: genomic sequence defines new  
variation spanning the nonclassical class I genes  
JOURNAL Unpublished  
2 (bases 1 to 5574)  
REFERENCE Ishihara, A., Miki, A., Williams, L.M., Moore, Y. and Geraghty, D.E.  
AUTHORS Direct Submission  
TITLE Submitted (21-JUN-2002) Clinical Division, Fred Hutchinson Cancer  
JOURNAL Research Center, 1100 Fairview Ave. N., D4-100, Seattle, WA  
98109-1024, USA

FEATURES  
source  
Location/Qualifiers  
1..5574  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="HOM2"  
/gene="HLA-G"  
/allele="HLA-G\*01011"  
/join(<1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3766,4123..>4127)  
/gene="HLA-G"

/product="MHC class Ib antigen"  
Join(1202..1274,1404..1673,1900..2175,2775..3050,  
3173..3289,3735..3739)  
/gene="HDA-G"  
/codon\_start=1  
/product="MHC class Ib antigen"  
/protein\_id="AA074999.1"  
/db\_xref="GI:21686652"  
/translation="NYVMAPIFLILSLALITLFTWAGSHSRKRYSAVSRGKEP  
RFLAMGYVDIDTFVRPDSACPRMEPRAPWQEQPEYEEETRNTHKAQIDRNL  
QILRGYVNDSEASHTLQWMAIGDLGSDRLJGQYAYDGDYDALNEDLSMTAA  
DTPAAOISKRKCEANVAEORRAYLEGGCEMLRLRYLENGKEMLRADPKPTHHPV  
FDYEATLRCAALCFYPAELITLWQRDGEPDQVLETPVEMDGRFOMAAVYVSG  
EDQRITCHVQHEILPEPLMRKQSSLPITPIINGIYAGLVIAAVTGAANAVLMRK  
KSSD"

BASE COUNT 1236 a 1438 c 1531 g 1364 t 5 others  
ORIGIN

Query Match 98.0%; Score 2392.2; DB 9; Length 5574;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2417; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 1 TACATCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGAGACCCCGACACCTC 60  
DB 1739 TACTGCCAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGAGACCCCGACACCTC 1798  
QY 61 TACCTGGAGAACCCCAAGGCGCTTTACAAAATCCCGCGGGTGGGTCCGGCGAGGG 120  
DB 1799 TACCTGGAGAACCCCAAGGCGCTTTACAAAATCCCGCGGGTGGGTCCGGCGAGGG 1858  
QY 121 CGAGGCTGGTGGGCGGGGCGAGCGAGGGGGGCGAGGTTCTCCACACCTCCAGTG 180  
DB 1859 CGAGGCTGGTGGGCGGGGCGAGCGAGGGGGTGGGCGAGGTTCTCCACACCTCCAGTG 1918  
QY 181 GATGATGGCTGCGACTGTGGGGTCCGAGCGAGCGCTCTCCGCGGGATGAAGATATGC 240  
DB 1919 GATGATGGCTGCGACTGTGGGGTCCGAGCGAGCGCTCTCCGCGGGATGAAGATATGC 1978  
QY 241 CTACGATGGCAAGATTACCTCGCCCTCAACGAGGACCTGGCTCTGGACCGCAGCGGA 300  
DB 1979 CTACGATGGCAAGATTACCTCGCCCTCAACGAGGACCTGGCTCTGGACCGCAGCGGA 2038  
QY 301 CACTCGGCTCGATCTCCCAAGCGCAAGTGTAGGCGGCGCAATGGGCTGAACAAAGAG 360  
DB 2039 CACTCGGCTCGATCTCCCAAGCGCAAGTGTAGGCGGCGCAATGGGCTGAACAAAGAG 2098  
QY 361 AGCTTACTGAGAGGCGAGTGGCTGAGTGGCTCCACAGATACCTGAGAAAGGGAGGA 420  
DB 2099 AGCTTACTGAGAGGCGAGTGGCTGAGTGGCTCCACAGATACCTGAGAAAGGGAGGA 2158  
QY 421 GATGCTGCAGCGCGGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTGTAGACCT 480  
DB 2159 GATGCTGCAGCGCGGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTGTAGACCT 2218  
QY 481 CTACAGCTGGGCTTACACAAAGGAGAGGAATGGGAGCAACACTGGAATATAGGCTT 540  
DB 2219 CTACAGCTGGGCTTACACAAAGGAGAGGAATGGGAGCAACACTGGAATATAGGCTT 2278  
QY 541 CCTCTGCTCTGAGGAGAGGAATCTCTGCTGTTTCCAGATCTCTGTAACGAGAGATGA 600  
DB 2279 CCTCTGCTCTGAGGAGAGGAATCTCTGCTGTTTCCAGATCTCTGTAACGAGAGATGA 2338  
QY 601 TTCTGAGGGCCGCTCTGCTCTCTGGACAAATTAAAGGATGAAGTCTCTGAGGAGTGA 660  
DB 2339 TTCTGAGGGCCGCTCTGCTCTCTGGACAAATTAAAGGATGAAGTCTCTGAGGAGTGA 2398  
QY 661 GGGGAAGACAAATCCGGAAGAGTATCAGGGGTTCCCTTGAACCCAGAGAGCTTGG 720  
DB 2399 GGGGAAGACAAATCCGGAAGAGTATCAGGGGTTCCCTTGAACCCAGAGAGCTTGG 2458  
QY 721 CACCAAGACTTTTCCCTCAGGCTTGTCTCTGCTCACAATCAATGTGTGGGGGTC 780  
DB 2459 CACCAAGACTTTTCCCTCAGGCTTGTCTCTGCTCACAATCAATGTGTGGGGGTC 2518

QY 781 TGACTCCAGCTCCTCTGAGTCCCTTGGCCTCCACTCAGGTCGAACCGGAGGTCCCTGCT 840  
DB 2519 TGACTCCAGCTCCTCTGAGTCCCTTGGCCTCCACTCAGGTCGAACCGGAGGTCCCTGCT 2578  
QY 841 CCCCCCTCAGAGACTAGAACTTTCACAAAGAAATAGAGATTAATCCAGGTCCCGTGTCC 900  
DB 2579 CCCCCCTCAGAGACTAGAACTTTCACAAAGAAATAGAGATTAATCCAGGTCCCGTGTCC 2638  
QY 901 AGGCTGTGTCTGGGTTCTGTGTGTCTCCCTTCCACCCAGGATATGTGTCTTACTTGG 960  
DB 2639 AGGCTGTGTCTGGGTTCTGTGTGTCTCCCTTCCACCCAGGATATGTGTCTTACTTGG 2698  
QY 961 ATGGTCAATCCAGGTGCTGCTGAGTGTCCCATGAGATGCAAAAGTCTGAATTTTC 1020  
DB 2699 ATGGTCAATCCAGGTGCTGCTGAGTGTCCCATGAGATGCAAAAGTCTGAATTTTC 2758  
QY 1021 TGACTCTTCTTTCAGACCCCTCCCAAGACACAGTACACACCTGTCTTGTACTAT 1080  
DB 2759 TGACTCTTCTTTCAGACCCCTCCCAAGACACAGTACACACCTGTCTTGTACTAT 2818  
QY 1081 GAGGCACTCTGAGT 1140  
DB 2819 GAGGCACTCTGAGT 2878  
QY 1141 CAGCGGATGGGGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1200  
DB 2879 CAGCGGATGGGGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2938  
QY 1201 GATGGAACCTTTCAGAAAGTGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260  
DB 2939 GATGGAACCTTTCAGAAAGTGGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2998  
QY 1261 ACGTGCATGTGACATATGAGGGGCTCCGACCCCTCAATGTGATGATGATGAGAG 1320  
DB 2999 ACGTGCATGTGACATATGAGGGGCTCCGACCCCTCAATGTGATGATGATGAGAG 3058  
QY 1321 GGAGATGAGGACATCATGTGTGTGAGAAAGAGAGAGGCTCTGTGAAGACCTTTAAACAG 1380  
DB 3059 GGAGATGAGGACATCATGTGTGTGAGAAAGAGAGAGGCTCTGTGAAGACCTTTAAACAG 3118  
QY 1381 GGTGCGTGTGAGGGCTGGGGGCTCAGAGACCTTCACCTCTTCTCCAGAGACAT 1440  
DB 3119 GGTGCGTGTGAGGGCTGGGGGCTCAGAGACCTTCACCTCTTCTCCAGAGACAT 3178  
QY 1441 CTTCCCTGCCACCATATCCCATATATGGGTATCGTGTGTGCTGGCTGTGCTTCCAGCTG 1500  
DB 3179 CTTCCCTGCCACCATATCCCATATATGGGTATCGTGTGTGCTGGCTGTGCTTCCAGCTG 3238  
QY 1501 TAGTCACATGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
DB 3239 TAGTCACATGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3298  
QY 1561 GGGTGACAAAGTGGGCTGTGAGTTTCTGTGCCACTGGGGGTTTCAAGCCCCAGAGTAA 1620  
DB 3299 GGGTGACAAAGTGGGCTGTGAGTTTCTGTGCCACTGGGGGTTTCAAGCCCCAGAGTAA 3358  
QY 1621 GTGTGCCCTGCTGT 1680  
DB 3359 GTGTGCCCTGCTGT 3418  
QY 1681 CCTGTGTGCCAGACCTTCTCTTTTGAAGACCTGTGACATGAAGAGAGATTTAT 1740  
DB 3419 CCTGTGTGCCAGACCTTCTCTTTTGAAGACCTGTGACATGAAGAGAGATTTAT 3478  
QY 1741 TACCTTGATATGTAGTATGGGACCTGATCCAGTAATCAGAGTCAAGAGAGGTC 1800  
DB 3479 TACCTTGATATGTAGTATGGGACCTGATCCAGTAATCAGAGTCAAGAGAGGTC 3538  
QY 1801 CCTGGCTAAGACAGACTTATGAGAGGCAAGTGTGTGAGAGCCCAATCTGTGCTTCTTG 1860  
DB 3539 CCTGGCTAAGACAGACTTATGAGAGGCAAGTGTGTGAGAGCCCAATCTGTGCTTCTTG 3598

CDs	1236 a	1438 c	1531 g	1364 t	5 others
CDs	1236 a	1438 c	1531 g	1364 t	5 others
BASE COUNT	1236 a	1438 c	1531 g	1364 t	5 others
ORIGIN	1236 a	1438 c	1531 g	1364 t	5 others
Query Match	98.0%	Score 2392.2	DB 9	Length 5574	
Best Local Similarity	99.8%	Pred. No. 0			
Matches 2417	Conservative 0	Mismatches 3	Indels 3	Gaps 2	
1	TACCTCCGAGTCTCCGGGCTGTGGATTCACCCGACGGCGGGGACCCGCGCCAGACCCCTC	60			
1739	TACTCCCGAGTCTCCGGGCTGTGGATTCACCCGACGGCGGGGACCCGCGCCAGACCCCTC	1798			
61	TACCTGGAGAACCCCAAGGCGCTTTACCAAAATCCCGCGGGGTGGTCCGGCGAGGG	120			
1799	TACTGGAGAACCCCAAGGCGCTTTACCAAAATCCCGCGGGGTGGTCCGGCGAGGG	1858			
121	CGAGGCTCGGTGGCGGGGCTGACCGAGAGGGGTGGGGCCAGGTTTCACACCCCTCAGTG	180			
1859	CGAGGCTCGGTGGCGGGGCTGACCGAGAGGGGTGGGGCCAGGTTTCACACCCCTCAGTG	1918			
181	GATGATTTGGCTGCGACCTTGGGCTCCGACGACGCGCTCTCTCCGGGTATGAACAGTATGC	240			
1919	GATGATTTGGCTGCGACCTTGGGCTCCGACGACGCGCTCTCTCCGGGTATGAACAGTATGC	1978			
241	CTACGATGCGAAGATATACCTGCGCTTCAACGAGAGACTCGCTCTGAGACGCAATCGA	300			
1979	CTACGATGCGAAGATATACCTGCGCTTCAACGAGAGACTCGCTCTGAGACGCAATCGA	2038			
301	CACCTGGGCTCAGATCTCCAAAGCAGATGTGAGAGCGGCCAATGTGGCTGAAACAAAGAG	360			
2039	CACCTGGGCTCAGATCTCCAAAGCAGATGTGAGAGCGGCCAATGTGGCTGAAACAAAGAG	2098			
361	AGCCTACCTGAGAGGACAGTGGTGGATGCTCCACAGATACCTGGAGAACGGGGAAGA	420			
2099	AGCCTACCTGAGAGGACAGTGGTGGATGCTCCACAGATACCTGGAGAACGGGGAAGA	2158			
421	GATGCTGACAGCGCGGCTACAGAGGAGAGTGGGGCGCTCCTGATCTCTGTAGACTT	480			
2159	GATGCTGACAGCGCGGCTACAGAGGAGAGTGGGGCGCTCCTGATCTCTGTAGACTT	2218			
481	CTACGCTGAGCTAGACACAGAGAGAGAAATGGGACCAACACTAGAAATATAGCCCT	540			
2219	CTACGCTGAGCTAGACACAGAGAGAGAAATGGGACCAACACTAGAAATATAGCCCT	2278			
541	CCCTCTGGTCTGAGAGAGAGAAATCCCTCCGCTTTCCAGATCTCTGACAGAGATGA	600			
2279	CCCTCTGGTCTGAGAGAGAGAAATCCCTCCGCTTTCCAGATCTCTGACAGAGATGA	2338			
601	TTCTGAGAGCCGCTCTCTGAGAGCAATTAAGGATGAAGATCTGAGAGAGTGA	660			
2339	TTCTGAGAGCCGCTCTCTGAGAGCAATTAAGGATGAAGATCTGAGAGAGTGA	2398			
661	GGGGAAGACAAATCCCTGGAGAGCTGATGAGGGTTCCCTTTAGACCCACAGACGCTTGG	720			
2399	GGGGAAGACAAATCCCTGGAGAGCTGATGAGGGTTCCCTTTAGACCCACAGACGCTTGG	2458			









GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 00:06:18 : Search time 158 Seconds  
(without alignments)  
6943.700 Million cell updates/sec

Title: US-09-622-846-16

Perfect score: 2442  
Sequence: 1 tactcccgagctctccggggtc.....ttgtcaatgccttccttg 2442

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551.6	63.5	4316	10 US-09-880-107-3713	Sequence 3713, App
2	513.2	21.0	1389	12 US-10-044-090-577	Sequence 577, App
3	496.4	20.3	1155	12 US-10-044-090-562	Sequence 562, App
4	461.2	18.9	466	10 US-09-864-761-737	Sequence 737, App
5	461.2	18.9	466	10 US-09-864-761-738	Sequence 738, App
6	429.2	17.6	600	9 US-09-964-261-396	Sequence 396, App
7	429.2	17.6	600	9 US-09-964-261-407	Sequence 407, App
8	427.6	17.5	600	9 US-09-964-261-397	Sequence 397, App
9	426	17.4	600	9 US-09-964-261-398	Sequence 398, App
10	421.2	17.2	600	9 US-09-964-261-405	Sequence 405, App
11	421.2	17.2	600	9 US-09-964-261-406	Sequence 406, App
12	410.8	16.8	599	9 US-09-964-261-399	Sequence 399, App
13	408.8	16.7	412	10 US-09-864-761-4806	Sequence 4806, App
14	406.8	16.7	598	9 US-09-964-261-444	Sequence 444, App
15	402.4	16.5	579	9 US-09-964-261-402	Sequence 402, App
16	400.8	16.4	579	9 US-09-964-261-403	Sequence 403, App
17	397.6	16.3	579	9 US-09-964-261-401	Sequence 401, App
18	385.2	15.8	577	9 US-09-964-261-400	Sequence 400, App
19	374.8	15.3	467	10 US-09-864-761-2470	Sequence 2470, App

C	20	363	14.9	478	10 US-09-864-761-735	Sequence 735, App
	21	355.2	14.5	574	9 US-09-964-261-445	Sequence 445, App
	22	348.8	14.3	470	10 US-09-864-761-2148	Sequence 2148, App
	23	347.2	14.2	574	9 US-09-964-261-404	Sequence 404, App
	24	347.2	14.2	574	9 US-09-964-261-410	Sequence 410, App
	25	344.2	14.1	575	9 US-09-964-261-415	Sequence 415, App
	26	344.2	14.1	575	9 US-09-964-261-424	Sequence 424, App
	27	344.2	14.1	575	9 US-09-964-261-428	Sequence 428, App
	28	344.2	14.1	575	9 US-09-964-261-429	Sequence 429, App
	29	342.6	14.0	575	9 US-09-964-261-416	Sequence 416, App
	30	342.6	14.0	575	9 US-09-964-261-417	Sequence 417, App
	31	342.6	14.0	575	9 US-09-964-261-418	Sequence 418, App
	32	341	14.0	575	9 US-09-964-261-409	Sequence 409, App
	33	341	14.0	575	9 US-09-964-261-412	Sequence 412, App
	34	340.8	14.0	587	9 US-09-964-261-441	Sequence 441, App
	35	340.8	14.0	587	9 US-09-964-261-446	Sequence 446, App
	36	339.4	13.9	575	9 US-09-964-261-411	Sequence 411, App
	37	339.4	13.9	575	9 US-09-964-261-425	Sequence 425, App
	38	339.2	13.9	587	9 US-09-964-261-431	Sequence 431, App
	39	339.2	13.9	587	9 US-09-964-261-432	Sequence 432, App
	40	339.2	13.9	587	9 US-09-964-261-436	Sequence 436, App
	41	339.2	13.9	587	9 US-09-964-261-440	Sequence 440, App
	42	337.8	13.8	575	9 US-09-964-261-426	Sequence 426, App
	43	337.6	13.8	587	9 US-09-964-261-430	Sequence 430, App
	44	337.6	13.8	587	9 US-09-964-261-433	Sequence 433, App
	45	337.6	13.8	587	9 US-09-964-261-434	Sequence 434, App

ALIGNMENTS

RESULT 1  
US-09-880-107-3713  
Sequence 3713, Application US/09880107  
Patent No. US20020142981A1  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Vockley, Joseph G.  
APPLICANT: Scherf, Uwe  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880,107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211,379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 3713  
LENGTH: 4316  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X17093  
US-09-880-107-3713  
Query Match 63.5%, Score 1551.6, DB 10, Length 4316;  
Best Local Similarity 82.7%, Pred. No. 0;  
Matches 2052; Conservative 0; Mismatches 344; Indels 84; Gaps 21;  
QY 1 TACTCCGAGCTCCGGGCTGGATCCACCCGAGCGCGGAGACCCGACAGACCTC 60  
DB 1377 TCCCGCCGAGTCTCCGATCCGAATACCCCGAGGAGC-GGACCCGCGCCAGACCTC 1435  
QY 61 TACTCCGAGAACCCCAAGGCGCTTTA-----CCAAATCC 98  
DB 1436 CACCCGGAGAGTCCACGCGCGCTTACCGAGGTCATTTCAGTTAGGCGCAAAATCC 1495  
QY GCGGGTGGCTCCGGGCGAGCGCTGGTGGCGGCGTGCACGAGGCGTGGGCG 158  
DB 1496 CCGGGTGGCGGGGAGGGGCGGGGCTAGCTGGGCGGGGCTGACTG-CGGGAGCGGC 1554



QY	Db
2446	3689
3749	
2405	
3809	

## RESULT 2

```

Sequence 577 Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 577
LENGTH: 1369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1382902.19
US-10-044-090-577

```

Query Match	21.0%;	Score 513.2;	DB 12;	Length 1389;
Best Local Similarity	88.1%;	Pred. No. 1.4e-138;		
Matches 627; Conservative	0;	Mismatches 78;	Indels 7;	Gaps 6

QY	602	TTGAGGGCCCGCTCCGTCGTCGAGACAAATTAAAGGATGAAAGTCCTCGAGGGAGAGG	661
Db	60	TTGAGAGGGCCCTCTTCTCTCT - AGCAATATTAAAGATGACGTCTCTGAGAAATGGAG	118
QY	662	GGGAGACAAATCCCTGGAAAGCATGATCAGGGGTTCCCTTTGACCC - ACAGACGCTT - G	719
Db	119	GGGAGACAGTCCCTAGAAATACGTATCAGGGGGTCCCTTTGACCCCTGACGACGCTTGG	178
QY	720	GCAACAGACATTTTCCCTCAGAGGCTTGTCTCTGCTACACATCATGTCTGGGGST	779
Db	179	GAAACCGTCACTTTTCTTCTCAGGCGCTTGCTCTCTGCTACACATGAGTGTGGGGCT	238
QY	780	CTACACTCGACGTCCTCTAGTCGCTTGCGCCCTCCTCAGTCAGGTAACGGAGCTCCCTGC	839
Db	239	CTGATTCAGACATCTCTGATGCATCTTACCTCCACTCAGATCAGAGAGAGAGTCCCTG -	297
QY	840	TCCCGCGGCTCAAGACATGAACTTTCCAGAGAAATAGAGATTAATCCAGAGTGGCCGTGTC	899
Db	298	TTCCCGGCTCACAAGCATGAACTTTCCAAAGAAATAGAGAAATTAATCCAGAGGCGCTCGTC	357
QY	900	CAGGCTGATGTGGATTCCTGCTCTGCTCCCTCCACCCAGGATATCTTGTTCAATCTTAG	959
Db	358	CAGGCTGATGTGGATTCCTGCTGTC - CCTTCCCAACCCAGAGTGACCTGCTCAATCTTAG	416
QY	960	GATGTGCATATCAGAGTCTCTGGAATGTCGATGCCATCAGAGATGCAAAAGTCTGAAATTTT	1011
Db	417	GCTGTGTCATCT - GGATGTGCTCTAGGGTGTGCCATATGAAGATGCAAAAGCGCTGAATTTT	474
QY	1020	CTGACTCTTCTTTAGACGCCGCCCAAGACACAGTCGACCCACACCCGCTCTTAGTA	1073
Db	475	CTGACTCTTCTTCCATCAGACGCCGCCCAAGACACAGTCGACCCACACCCGCTCTTAGTA	534
QY	1080	TGAGGCCACCCAGAGTCTCTGAGGCCCTGAGGCTCTTACCTCTGGAGATCAATCTGACCTG	1133
Db	535	TGAGGCCACCCAGAGTCTCTGAGGCCCTGAGGCTCTTACCTCTGGAGATCAATCTGACCTG	594

QY	1140	GCAGCGGATATGGGAGGAGACACCAAGACCAGAGACCTGTGGAGCTCTGGAGAGACAGGCGCTTGGAG	1199
Db	595	GCAGCGGATATGGGAGGAGACCAAACTCAGAGCACTGTGAGCTTGTGGAGACACAGACACCGCAGCAG	654
QY	1200	GGATGGAACCTTTCAGAAAGTGGGAGAGTGTGGTGGTGGCTTCGAGAGAGAGGAGACACAGATA	1259
Db	655	AGATGGAACCTTTCAGAAAGTGGGAGAGTGTGGTGGTGGCTTCGAGAGAGAGACACAGAGATA	714
QY	1260	CACGCGGCATGTGCAGCATATGAGGGGGTGGCCGGAGGCCCTCATGTGAGATGG	1311
Db	715	CACATGCCATTTACAGCATATGAGGGGGTGGCCGGAAGGCCCTCATACCTGAGATGG	766

### RESULT 3

```

: Sequence 562, Application US/10044090
: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: CURRENT FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: PERL Program
: SEQ ID NO: 562
: LENGTH: 1155
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020137081A1 1383423.1
: NAME/KEY: unsure
: LOCATION: 344..394
: OTHER INFORMATION: a, t, c, g, or other
:
: US-10-044-090-562

```

Query Match	20.38;	Score 496.4;	DB 12;	Length 1155;
Best Local Similarity	81.68;	Pred. No. 9.4e-134;		
Matches 668; Conservative	0;	Mismatches 122;	Indels 29;	Gaps 7,

OY	135	GGCAGAGCTTCACACCCCTCCAGTGGATGATGTTGGCGGAGACTGGGGTCCGACGGACGC	214
Db	346	GAGGCGCGGGTCTCACACCTCCAGAAATATATATGGCTGGGACTGGGGCCGACGGGCGC	405
OY	215	CTCTCCGCGGGATTAACAGATATGCCCTACAGATGGCAAGGATTTACTCTGGCCCTGAACGAG	274
Db	406	CTCTCCGCGGGATATGACGAGGCCCTACGAGGCAAGGATTTACTATCGCCCTGAACGAG	465
OY	275	GACCTGGCGCTCCT-GGACCCGACGGCGGACACTGGGGCTCAGATCTCCAAAGGCCAAGTGTGA	333
Db	466	GACCTGGAGCTCCGGGAGCCGCGCGGACACCGCGGCTCAGATCCACGAGCCAAAGTGTGA	525
OY	334	GGCGCCAAATGTGGCTGAGACAAGGAGAGGCTACCTAGTGGAGGCGACGTCGTCGGATGGCT	393
Db	526	GGCGCCCGGCTGTGGCGGACAGGACAGAGGCTTACTGAGAGGGGAGTGCCTGGATGGCT	585
OY	394	CCACAGATACCTGGAGACGGGAGAGGATGCTGACGCGCGGGTACCAGGGCCATGG	453
Db	586	CCGAGATACCTGGAAACGGGAAAGCAACACCTGAGCGCGCTGTACCAAGGGCCACTGG	645
OY	454	GGCGCTCCCTGATCTCTGTAGACACCTTCAGCTGCGGCTACAGCAAGGAGAGGAGAAA	513
Db	646	GGAGGCTTCCCATCTCTATATAGTGGCGGGGATGSGCTCCGACGAAAGAGGAGGAAA	705
OY	514	ATGGGACCAACACTAGAAATATCGCCCTCCTCTGGTCTCTGAGGAGAGGAAATCCTCTGG	573
Db	706	ATGGGATACACGCTAAGAAATGTGGCCCTCCGTGAATGAGAAATGGCAATGAGTTTCTCGA	765
OY	574	GTTTTCAGATATCTGTACGAGAGATGATTTGAGAGGCGCGCTCGCTGCTCTGGGACAAAT	633
Db	766	GTITTC-----TCTGAGGGCGCCCTTCTCTCTAGA--CAAT	801

```

CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263,6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30

```

```

RESULT 5
US-09-664-761-738/c
: Sequence 738, Application US/09664761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aeoimica-X-1
: CURRENT APPLICATION NUMBER: US/09/664,761
: CURRENT FILING DATE: 2001-05-23

```

```

; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 738
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023057.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2e+02
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1e+02
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 27
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 33
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 69
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1e+02
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 18
US-09-864-761-738

Query Match      18.9%; Score 461.2; DB 10; Length 466;
Best Local Similarity 99.4%; Pred. No. 8.9e-124;
Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

|||||
Db 286 GCGTCCGAGAGCCCTCATGCTAGATGAGTAAGAGGAGATGGAGCATCATGCTG 227
Qy 1343 TTAGGGAAGACAGAGCCTCTCTGAAGACCTTTAACAGGCTGGTGTAGGCTGGGG 1402
Db 226 TTAGGGAAGACAGAGCCTCTCTGAAGACCTTTAACAGGCTGGTGTAGGCTGGGG 167
Qy 1403 TCAGAGACCTCATGCTTCACTCCCTTCCAGAGCATGCTTCCCATCCCAT 1462
Db 166 TCAGAGACCTCATGCTTCACTCCCTTCCAGAGCATGCTTCCCATCCCAT 107
Qy 1463 CATGGATGATGCTTGAGCCTGGTGTCTTGCAGCTGATGACTGAGCTGGCTGC 1522
Db 106 CATGGATGATGCTTGAGCCTGGTGTCTTGCAGCTGATGACTGAGCTGGCTGC 47
Qy 1523 TCCTGTCTGTGAGGAAGAGCTCAGCTAGAGAGGGGTGACA 1568
Db 46 TCCTGTCTGTGAGGAAGAGCTCAGCTAGAGAGGGGTGACA 1

RESULT 6
US-09-964-261-396
; Sequence 396, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: Rombout, Annelles
; APPLICANT: Kossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 396
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-396

Query Match      17.6%; Score 429.2; DB 9; Length 600;
Best Local Similarity 86.4%; Pred. No. 1.9e-114;
Matches 522; Conservative 0; Mismatches 73; Indels 9; Gaps 4;
```

Db	360	TTTCGATGTCCTCAGCCTCCACTCAGGTACGACACAGAGAGTGCATGTTCCCTC--TTTCAG	418
Qy	853	GACTAGAACTTTCACAGSAAATAGAGATTAATCCACAGTCCCGTTCACAGCGTGGTCT	912
Db	419	GACTAGAAATTTTCCACGGAATTAGAGATTTATCCAGAGTCCCTGTCCACAGCTGGTCTCT	478
Qy	913	GGGTTCTGTGCTCCCTTCCACCCACCGATATCTGGTTCAATCTTAGATGAGTGCACATCC	972
Db	479	GGGTTCTGTGCTCCCTTCCACCCACCGAGTGTCTTCATTTCTCAAGATACCCACAT--	536
Qy	973	AGGTGTCTGTGAGATGTCCCATGAGAGATGCAAAAGTCTTGAAATTTTTCGACTCTTCTT	1032
Db	537	GTTGTCTGTGAGAGATGTCCCATGACATGACAAATATGCTGTAATGTTTGTACTCTTCTGT	596
Qy	1033	TTCAAG	1036
Db	597	ACAG	600

```

RESULT 7
US-09-964-261-407
Sequence 407, Application US/09964261
Publication NO. US20020197613A1
GENERAL INFORMATION:
APPLICANT: De Canck, Ilse
APPLICANT: Rombout, Annelies
APPLICANT: Rossau, Rudi
TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
FILE REFERENCE: IGA-002
CURRENT APPLICATION NUMBER: US/09/964,261
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: EP 93870068.6
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/138,614
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 407
LENGTH: 600
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-261-407

```

[illegible]

Db	360	TTCTAGACCTCCAGCTCCACTAGATCGAGGACGAGAAAGTGCCTGTCCCTC	-TTCAAG	418
QY	853	GACTAGAACTTTCCAAAGAAATAGAGATTATCCACAGTCCCGTGCACGGCTGTC		912
Db	419	GACTAGATTTTCCACGSAATAGAGATTATCCACAGTGCCTGTCTCCAGGCTGGTCT		478
QY	913	GAGTTCTGTGCTCCCTTCCGCCACCCACGATATCGTTCAATTTAGATGGTCAATCC		972
Db	479	GGGGTCTGTGCTCCCTTCCGCCACCCACGATATCGTTCAATTTCAAGATATCCACAT--		536
QY	973	AGGTGCTCTGGAGTGTCCCATAGAGATCAAAAGTCTGGAATTTTGCAGCTTTCCTT		1032
Db	537	GTTGTCTGGAGATGTGCCATGACAAATATGCCATGTAATGTTCAGCTTTCCTG		596
QY	1033	TCAG	1036	
Db	597	ACAG	600	

```

? RESULT 8
? US-09-964-261-397
? Sequence 397, Application US/09964261
? Publication No. US20020197613A1
? GENERAL INFORMATION:
? APPLICANT: De Canck, Ilse
? APPLICANT: Rombout, Annelies
? APPLICANT: Rossau, Rudi
? TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
? FILE REFERENCE: IGI-002
? CURRENT APPLICATION NUMBER: US/09/964,261
? CURRENT FILING DATE: 2001-09-25
? PRIOR APPLICATION NUMBER: EP 99670068.6
? PRIOR FILING DATE: 1999-04-09
? PRIOR APPLICATION NUMBER: US 60/138,614
? PRIOR FILING DATE: 1999-06-11
? NUMBER OF SEQ ID NOS: 446
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 397
? LENGTH: 600
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-964-261-397

```

Query Match	17.5%:	Score 427.6:	DB 9:	Length 600:
Best Local Similarity	86.3%:	Pred. No. 5.7e-114:		
Matches 521:	Conservative	0:	Mismatches 74:	Indels 9:
			Gaps	4:
QY 438	GTACAGAGGGCAGTGGGGGCGCCCTCCCTGATCTCTGTAGACCTCTCAGACCTCGGCGCTTAGCA	497		
Db 1	GTACACAGGGGCGCACAGAGGCGCCCTCCCTGATCGCTGTGTAGATCTCCGGGCGTGGCGCTTCCA	60		
QY 498	CAGAGAGAGGAGGAAATGGGACCAACTAGATATATGCGCCCTCCCTCTGCTCTAGGG	557		
Db 61	CAGAGAGGAGGAGCAATGGGAGCAACTAGATATATGCGCCCTCCCTCTGCTCTAGGG	120		
QY 558	AGAGAAATCTCTCTGGGTTCTTCAGATCTCTGTACAGAGAGATGTATGAGGGCCCGCTT	617		
Db 121	AGAGAAATCTCTCTGGGTTCTTCAGATCTCTGTACAGAGAGATGTATGAGGGTTCCGGCT	180		
QY 618	GCTCTCTGGGACATTTAAGGATGAAGTCTCTGAGGAGTGGAGGAGACATTCCTCTG	677		
Db 181	GCTCTCTGGGACATTTAAGGATGAAGTCTCTGAGGAGT--GAGCGGAGAGCGATCTCTCTG	239		
QY 678	GAGACGTGATCAGAGGGGTTCCCTTTGAC-----CCACAGACGAGCCCTGGACACAGAGACTTT	732		
Db 240	GAAATCTGATGAGGGTTCCTTTTGACACACACCGGAGCGACCTTGGGCCCTGATCTT	299		
QY 733	TCCCTCAGGCGCTTGTCTCTGCTCTCACACTCAATGTGTGAGGGGAGTGTGATCTACAGCTC	792		
Db 300	TCTCTCAGGCGCTTGTCTCTGCTCTCACACTCAATGTGTGAGGGGAGTGTGATCTACAGCAC	359		
QY 793	CTTGATTCCTTGGCCTCACTCAGGTAGAACCGGAGGATTCCTGCTCCCCCGGCTCAGA	852		

D <sub>b</sub>	360	TTCTGATGCTCCCTAAGGCTCCACGTCAAGGTGAGGACCAAGAAAGTCGCTGTGCCCTC - TTCAAG	418
O <sub>Y</sub>	853	GACTAGACATTTTCCAGGAAATAGAGATTAATCCAGAGTCCCGTCCAGGCTGSGTCT	912
D <sub>b</sub>	419	GACTAGAAATTTTCCACGAGATAGGAAATTATCCCAAGTCCCTGTGTTCCAGGCTGTGCT	478
O <sub>Y</sub>	913	GGGTTCTGTCTCCCTCCCTCCACCCAGGTATCTGGTTCAATCTTAAAGATGGTCACATCC	972
D <sub>b</sub>	479	GGGTTCTGTCTCCCTCCCTCCACCCAGGTTGTCCTCATTTCTCAAGTATACCACAT -	536
O <sub>Y</sub>	973	AGGTCGTCGTGAGATGTCCTCAGAGAGATCAAAAGTCTTGAAATTTTTCGACTCTTCCTT	1032
D <sub>b</sub>	537	GTGTGCTGGAGAGATGTCCCATCATCAGAAATGCAAAAGCTGAAATGTGTGACTCTTCCG	596
O <sub>Y</sub>	1033	TCAG	1036
D <sub>b</sub>	597	ACAG	600

```

RESULT 9
US-09-964-261-398
: Sequence 398, Application US/09964261
: Publication No. US20020197613A1
: GENERAL INFORMATION:
: APPLICANT: De Canck, Ilse
: APPLICANT: Rombout, Annelies
: APPLICANT: Rossau, Rudi
: TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
: FILE REFERENCE: IGT-002
: CURRENT APPLICATION NUMBER: US/09/964,261
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: EP 99870068.6
: PRIOR FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: US 60/138,614
: PRIOR FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 446
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 398
: LENGTH: 600
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-964-261-398

```

Query Match	17.4%	Score 426;	DB 9;	Length 600;
Best Local Similarity	86.18;	Pred. NO. 1.7e-113;		
Matches 520;	Conservative	0;	Mismatches 75;	Indels 9;
				Gaps 4;

Qy 438 GTTACAGGGGCGAGTGGGGGGGCGCTCCGATGCTTCTGTGAGACTCTCAGGCTGGCGTAGCA 497

Db 1 GTACCAAGGGGGCCACGGGGGGCGCTCCCTGTATGCTTGTAGATCTCCGGGGCTGGCTCCCA 60

Qy 498 CAAAGGAGAGAGGAGAAATGGGACCAACTAGAAATATCGCCCTCCCTGTGGTCCCTGAGGG 557

Db 61 CAAGGAGGGGGAGACATTTGGGACCAACTAGAAATATCGCCCTCCCTGTGGTCCCTGAGGG 120

Qy 558 AGAGGAATCTTCCTGGGTTTCCAGATCTGTACCAAGAGTGAATTTGTAGGGCCCGTCT 617

Db 121 AGAGGAATCTCTCTGGGTTTCCAGATCTGTACCAAGAGTGAATTTGTAGGGTTCCGGCT 180

Qy 618 GCTCTCTGGGACAATTAAGGATGAAGTCTGTAGGGAGTGGAGGAAAGACATCCCTG 677

Db 181 GCTCTCTGACAAATTAAGGATGAAGTCTGTAGGAGAT - GACGGGAAGCGATCCCTC 239

Qy 678 GAGACTGATACGGGGTTCCTTTAC-----CCACAGCAGCCTTGGACACAGACTTT 732

Db 240 GAATACTGATGATGGTTTCCCTTTACACACACAGCAGCAGCCTTGGGGCCCGACTTT 299

Qy 733 TCCCTTCAGGCGTTGTCTCTGCTGCCTACACTCAATGTGTGTGGGGTCTGACTCCAGCTC 792

Db 300 TCTCTTCAGGCGTTGTCTCTGCTTCACACTCAATGTGTGTGGGGTCTGTAGTCCAGAC 358

Qy 793 CTCTGATCCCTTGGCTTCACCTCAGGTCAGATCCGAGACCGGAGTCCCTGCTCCCCCGCTCAGA 85

Db	360	TTTCGATTCCTCCAGCTCCAGCTCCAGTCCAGGACGAGAGTGCCTGTTCCCTC--TTGAGG	418
QY	853	GACTAGAACATTTTCCAGGAATAGGAATATTTCACAGTCCCGTCTCCAGGCTGGTGTCT	912
Db	419	GACTAGAAATTTTCCAGGAATAGGAATATTTCACAGTCCCTGTGTCCAGGCTGGTGTCT	478
QY	913	GGGTTCTGTGTGCTCCCTCCCTCCACCCAGGATCTGTTCAATCTTAGAGATGTCACATCC	972
Db	479	GGGTTCTGTGTGCTCCCTCCCTCCACCCAGGATGTCCTTCATTTCTAAAGTATCCACAT--	536
QY	973	AGGTCCTGCTGGAATGTCCTCATGATGAGATGCAAAAGTCTTGAAATTTTCTGACTCTTTCCT	1032
Db	537	GTCGTCTGAGAGATGTTCATGATGACATGACAAATGCTGAAATGATCTGACTCTTTCCTG	596
QY	1033	TCAG	1036
Db	597	ACAG	600

```

RESULT 10
US-09-964-261-405
; Sequence 405, Application US/09964261
; Publication NO. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: IGT-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-405

```

Query Match	17.28;	Score 421.2;	DB 9;	Length 600;
Best Local Similarity	85.68;	Pred. No. 4.1e-112;		
Matches 517; Conservative	0;	Mismatches 78;	Indels 9;	Gaps 4;

Qy	438	GTCCAGGGGGGACAGTGGGGGGCCCTCCCTATGCTCCGTAGACATCTCGAGCTTCGGGCTCAGGA	497
Db	1	GTACCAGGGGGCCACAGGGGGGCTCCCTCTATGCTCTGATGCTCTCGAGCTTCGGGCTCAGGA	60
Qy	498	CAAGGAGAGAGGAAAAATGGAGCAACACTAGAAATATGCGCCCTCCCTGTGCTCTAGGG	557
Db	61	CAAGGAGGGGACACATTTGGAGCAACACTAGAAATATGCACTCCCTCTGTGCTCTAGGG	120
Qy	558	AGAGGAATCCTCCTGGGTTTCCAGATCCTGTACACAGAGATGATTTCTGAGGGCCCGCTT	617
Db	121	AGAGGAATCCTCCTGGGTTTCCAGATCCTGTACACAGAGATGATTTCTGAGGGTTCCGCTT	180
Qy	618	GCTCTCTGGACAAATTAAAGGAGTGAAGTCTGAGAGGAGTGGAGGAAAGATCCCTG	677
Db	181	GCTCTGTGAACAAATTAAAGGAGTGAAGGAGT-GAGGGGAAGCATCTCCCTC	239
Qy	678	GAGACAGTACAGGGGTTCCCTTTGAC-----CCACACAGACCTTGACACAGACTTT	732
Db	240	GAAATCTGATGATGGTTCTTCCTTTTGCACACACCGGACAGACCTTTGGGCCCGTACTTT	299
Qy	733	TGCCCTCAGGCGTTGTTTCTCTGCTCACAATCATGTGTGTGGGGTCTGACTCAGCTC	792
Db	300	TCTCTCAGGCGTTGTTTCTCTGCTTACACTCAATGTGTGTGGGGTCTGAGTCCAGACAC	359
Qy	793	CTCTGATCCTTTGGCTCCACTCAGGTGAGAACCGGAGTCCCTGCTCTCCCGGCTCAGA	855



```

|||||
Db 360 TTCTGAGTCCCTCAGACCTCCACTCAGGTCAGACAGCAAGTGGCTGTCCCTC-TCAGG 418
OY 853 GACTAGACTTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGTGTCT 912
Db 419 GACTAGAAATTTTCCAGGAATAGAGATTTATCCAGGTGGCTGTCCAGGCTGGTGTCT 478
OY 913 GGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 972
Db 479 GGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 536
OY 973 AGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 1032
Db 537 GTGTCTGTGAGAGTGTTCATTCAGATGTCGAATGTCCTGAATGTTCGACTCTTCG 596
OY 1033 TCAG 1036
Db 597 ACAG 600

```

```

RESULT 11
US-09-964-261-406
; Sequence 406, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ISJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 406
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-406

```

Query Match 17.2%; Score 421.2; DB 9; Length 600;  
 Best Local Similarity 85.6%; Pred. No. 4.1e-112;  
 Matches 517; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

```

OY 438 GTACCAGGGGAGTGGGGGCGCTCCGATCTCTGTAGACCTCTAGCCTGGCCTAGCA 497
Db 1 GTACCAGGGGAGTGGGGGCGCTCCGATCTCTGTAGACCTCTGGGCTGGCCTCCCA 60
OY 498 CAAGGAGAGAGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGGTCTGAGGG 557
Db 61 CAAGGAGAGAGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGGTCTGAGGG 120
OY 558 AGAGGATCTCTGCGGTTCCTGATCTCTGATCCAGAGATGATTTGAGGGCCCTGCT 617
Db 121 AGAGGATCTCTGCGGTTCCTGATCTCTGATCCAGAGATGATTTGAGGGCCCTGCT 180
OY 618 GCTCTCTGGGCAATTAAGGATGAAGTCTGTAGGAGTGGAGGGAGAGCAATCCCTG 677
Db 181 GCTCTCTGGGCAATTAAGGATGAAGTCTGTAGGAGTGGAGGGAGAGCAATCCCTG 239
OY 678 GAAGACTGATCAGGGGCTTCCTTTGAC-----CCACAGAGAGCTTTGGCACAGGACTTT 732
Db 240 GAATCTGATGAGTGGTTCCTTTGACACACACCGGAGAGAGCTTTGGGCGCTGACTTT 299
OY 733 TCCTCTCAGGGCTTTGCTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCTC 792
Db 300 TCCTCTCAGGGCTTTGCTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGC 359
OY 793 CTCGTGAGTCCCTTGGCCTCCACTCAGAGTCAAGAACGGAGGTCCCTGTCCCGGCTCAGA 852

```

```

|||||
Db 360 TTCTGAGTCCCTCAGACCTCCACTCAGTCCAGACAGAAAGTGGCTGTCCCTC-TCAGG 418
OY 853 GACTAGAACTTTTCCAGGAATAGAGATTTATCCAGGTGCCCGTCCAGCTGGTGTCT 912
Db 419 GACTAGAAATTTTCCAGGAATAGAGATTTATCCAGGTGGCTGTCCAGGCTGGTGTCT 478
OY 913 GGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 972
Db 479 GGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 536
OY 973 AGGTCTGTGCTCCCTTCCACCCAGGATGTCGTTCATTTCTAGAGTGTACATCC 1032
Db 537 GTGTCTGTGAGAGTGTTCATTCAGATGTCGAATGTCCTGAATGTTCGACTCTTCG 596
OY 1033 TCAG 1036
Db 597 ACAG 600

```

```

RESULT 12
US-09-964-261-399
; Sequence 399, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ISJ-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 399
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-399

```

Query Match 16.8%; Score 410.8; DB 9; Length 599;  
 Best Local Similarity 85.6%; Pred. No. 4.2e-109;  
 Matches 517; Conservative 0; Mismatches 77; Indels 10; Gaps 5;

```

OY 438 GTACCAGGGGAGTGGGGGCGCTCCGATCTCTGTAGACCTCTAGCCTGGCCTAGCA 497
Db 1 GTACCAGGGGAGTGGGGGCGCTCCGATCTCTGTAGACCTCTGGGCTGGCCTCCCA 60
OY 498 CAAGGAGAGAGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGGTCTGAGGG 557
Db 61 CAAGGAGAGAGAGAAATGGGACCAACACTAGATATCGCCCTCCCTGTGGTCTGAGGG 120
OY 558 AGAGGATCTCTGCGGTTCCTGATCTCTGATCCAGAGATGATTTGAGGGCCCTGCT 617
Db 121 AGAGGATCTCTGCGGTTCCTGATCTCTGATCCAGAGATGATTTGAGGGCCCTGCT 180
OY 618 GCTCTCTGGGCAATTAAGGATGAAGTCTGTAGGAGTGGAGGGAGAGCAATCCCTG 677
Db 181 GCTCTCTGGGCAATTAAGGATGAAGTCTGTAGGAGTGGAGGGAGAGCAATCCCTG 239
OY 678 GAAGACTGATCAGGGGCTTCCTTTGAC-----CCACAGAGAGCTTTGGCACAGGACTTT 732
Db 240 GAATCTGATGAGTGGTTCCTTTGACACACACCGGAGAGAGCTTTGGGCGCTGACTTT 299
OY 733 TCCTCTCAGGGCTTTGCTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGCTC 792
Db 300 TCCTCTCAGGGCTTTGCTCTGCTCAGCTCACTCAATGTGTGGGGGTCTGACTCCAGC 359
OY 793 CTCGTGAGTCCCTTGGCCTCCACTCAGAGTCAAGAACGGAGGTCCCTGTCCCGGCTCAGA 852

```



```
Db 360 TTCTGAGTCCCTCAGCCTCCAGCTAGGTCAGAGCCAGAAAGTCGCTGTCCCTC-TTCCAGG 418
      |||
Qy 853 GACTAGAACCTTCCAGAGATAGAGATTAATCCAGGTGCCCGCTGCAGCGTGCTCT 912
      |||
Db 419 GACTAGAA-TTCCACGAGATAGAGATTAATCCAGGTGCCCGCTGCAGCGTGCTCT 477
Qy 913 GGGTTCTGTGCTCCCTTCCACCCAGGTAATCTGTTTCAATCTTAGAGATGTCACATCC 972
      |||
Db 478 GGGTTCTGTGCTCCCTTCCACCCAGGTAATCTGTTTCAATCTTAGAGATGTCACATCC 535
Qy 973 AGGTGCTGCTGCTCCCTTCCACCCAGGTAATCTGTTTCAATCTTAGAGATGTCACATCC 1032
      |||
Db 536 GTGTGCTGAGAGATGTCACATGACAGATACCCCAATGCTGTATGTTCTGACTTCTCTG 595
Qy 1033 TCAG 1036
      |||
Db 596 TCAG 599

RESULT 13
US-09-864-761-4806/c
: Sequence 4806, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aecomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 4806
```

```
: LENGTH: 412
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AF055066.1
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 38
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 33
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 25
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 16
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.4
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.5
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 59
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 25
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
US-09-864-761-4806

Query Match 16.7%; Score 408.8; DB 10; Length 412;
Best Local Similarity 99.5%; Pred. No. 1.3e-108;
Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1075 GACTATGAGCCACCTCGAGAGTCTGGGCTTCTACCTCGGAGATCATCTG 1134
      |||
Db 412 GACTATGAGCCACCCCTGAGAGTCTGGGCTTCTACCTCGGAGATCATCTG 353
Qy 1135 ACCTGCGAGCGGGATGGGAGAGACACAGCCAGAGCTGAGCTCGTGAAGACGCT 1194
      |||
Db 352 ACCTGCGAGCGGGATGGGAGAGACACAGCCAGAGCTGAGCTCGTGAAGACGCT 293
Qy 1195 GCAGGGGATGAACCTTCCAGAAAGTGCGAGCTGTGGTGTGCTTCTGAGAGACAG 1254
      |||
Db 292 GCAGGGGATGAACCTTCCAGAAAGTGCGAGCTGTGGTGTGCTTCTGAGAGAGAG 233
Qy 1255 AGATACACGTGCTATGTCAGCATGAGGCTCCGAGCCCTCATGCGTGAATGAGT 1314
      |||
Db 232 AGATACACGTGCTATGTCAGCATGAGGCTCCGAGCCCTCATGCGTGAATGAGT 173
Qy 1315 AAGAGGAGATGAGAGCATCATGCTGTAGGAGAAAGCAGAGCCTCTCTGAAGACTT 1374
      |||
Db 172 AAGAGGAGATGAGAGCATCATGCTGTAGGAGAAAGCAGAGCCTCTCTGAAGACTT 113
Qy 1375 TAACAGGCTGGTGTGAGGCTGGGGCTGAGAGACCTTACCTTCTTCCAG 1434
      |||
Db 112 TAACAGGCTGGTGTGAGGCTGGGGCTGAGAGACCTTACCTTCTTCCAG 53
Qy 1435 AGCAGTCTCCCTGCCACCATCCCATCATGAGGTATGCTGGGCTGGT 1486
      |||
Db 52 AGCAGTCTCCCTGCCACCATCCCATCATGAGGTATGCTGGGCTGGT 1

RESULT 14
US-09-964-261-444
: Sequence 444, Application US/09964261
: Publication No. US20020197613A1
: GENERAL INFORMATION:
: APPLICANT: De Canck, Ilse
: APPLICANT: Rombout, Annelies
: APPLICANT: Rossau, Rudi
: TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
: FILE REFERENCE: IGJ-002
: CURRENT APPLICATION NUMBER: US/09/964,261
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: EP 99870068.6
: PRIOR FILING DATE: 1999-04-09
: PRIOR APPLICATION NUMBER: US 60/138,614
: PRIOR FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 446
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 444
: LENGTH: 598
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-964-261-444
```

Query Match 16.7%; Score 406.8; DB 9; Length 598;  
Best Local Similarity 86.3%; Pred. No. 6,1e-108;  
Matches 521; Conservative 0; Mismatches 72; Indels 11; Gaps 6;

```
QY 438 GTACACAGGGCAGTGGGGGCGCTCCCTGATCTCTGTAGACCTCTGACGCTGAGCTGACGA 497
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GTACACAGGGGCGACAGGGGCGCTCCCTGATCTCTGTAGATCTCCGGGCTGAGCTGACGA 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 498 CAGGAGAGGAGGAAATGGGACCAACATAGATATCCGCCCTCCCTGCTGCTCTGAGG 557
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CAGGAGGAGGAGACAAATTTGGGACCAACATAGATATCCGCCCTCCCTGCTGCTCTGAGG 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 558 AGAGGAATCTCTCTGGGTTTCAGATCTCTGTACAGAGATGATTTGAGGGCCCGCTCT 617
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 AGAGGAATCTCTCTGGGTTTCAGATCTCTGTACAGAGATGATTTGAGGGTTCCGCCCT 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 618 GCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAGGGAAGACAAATCCCTG 677
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 GCTCTCTGACACAAATTAAGGATGAAGTCTCTGAGGGAAT-GACGGGAAGACGATCCCTG 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 678 GAGACTGATCAGGGGTTCCCTTGAC-----CCACAGACGCTTGACACGACGCTTT 732
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 733 TCCCTCAGGCGCTTTCTCTCTGCTCAGACTCAATGCTGTGGGGGCTGAGCTCCAGCTC 792
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 300 TCCCTCAGGCGCTTTCTCTCTGCTCAGACTCAATGCTGTGGGGGCTGAGCTCCAGCTC 359
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 793 CTCTGAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGGCTCCCTGCTCCCGCTCAGA 852
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 360 TTCTGAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGGCTCCCTGCTCCCGCTC 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 853 GACTAGACTTTCCAGAGATAGAGATATCCAGAGTCCCGCTGCTGACGCTGGGCT 912
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 GACTAGACTTTCCAGAGATAGAGATATCCAGAGTCCCGCTGCTGACGCTGGGCT 478
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 913 GGGTTCTGCTGCTCCCTCCCAAGGATGCTGGTTCATTTAGATGCTGACATCC 972
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 479 GGGTTCTGCTGCTCCCTCCCAAGGATGCTGGTTCATTTAGATGCTGACATCC-- 536
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 973 AGGTGCTGGGAGTGTCCCATGAGAGATGCAAGGCTTGAATTTCTGATCTCTCTT 1032
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 537 GTGTGCTGGAGAGTGTCCCAT-ACAGATGCAAA-TGCTGATGCTGACTCTTCTG 594
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1033 TCAG 1036
   | | |
Db 595 ACAG 598
```

RESULT 15  
US-09-964-261-402  
; Sequence 402, Application US/09964261  
; Publication No. US20020197613A1  
; GENERAL INFORMATION:  
; APPLICANT: De Canck, Ilse  
; APPLICANT: Rombout, Annelies  
; APPLICANT: Rossau, Rudi  
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES  
; FILE REFERENCE: IGJ-002  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/964,261  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: US 60/138,614  
; PRIOR FILING DATE: 1999-06-11  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 402  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-261-402

Query Match 16.5%; Score 402.4; DB 9; Length 579;  
Best Local Similarity 84.5%; Pred. No. 1,1e-106;  
Matches 507; Conservative 0; Mismatches 71; Indels 22; Gaps 4;

```
QY 438 GTACACAGGGCAGTGGGGGCGCTCCCTGATCTCTGTAGACCTCTGACGCTGAGCTGACGA 497
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GTACACAGGGGCGACAGGGGCGCTCCCTGATCTCTGTAGATCTCCGGGCTGAGCTGACGA 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 498 CAGGAGAGGAGGAAATGGGACCAACATAGATATCCGCCCTCCCTGCTGCTCTGAGG 557
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CAGGAGGAGGAGACAAATTTGGGACCAACATAGATATCCGCCCTCCCTGCTGCTCTGAGG 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 558 AGAGGAATCTCTCTGGGTTTCAGATCTCTGTACAGAGATGATTTGAGGGCCCGCTCT 617
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 AGAGGAATCTCTCTGGGTTTCAGATCTCTGTACAGAGATGATTTGAGGGTTCCGCCCT 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 618 GCTCTCTGGGACAAATTAAGGATGAAGTCTCTGAGGAGTGGAGGGAAGACAAATCCCTG 677
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 GCTCTCTGACACAAATTAAGGATGAAGTCTCTGAGGGAAT-GACGGGAAGACGATCCCTG 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 678 GAGACTGATCAGGGGTTCCCTTGAC-----CCACAGACGCTTGACACGACGCTTTCC 736
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 737 CTGAGGCGCTTTCTCTCTGCTCAGACTCAATGCTGTGGGGGCTGAGCTCCAGCTCTCT 796
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 300 CTGAGGCGCTTTCTCTCTGCTCAGACTCAATGCTGTGGGGGCTGAGCTCCAGCTCTCT 359
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 797 GAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGGCTCCCTGCTCCCGCTCAGAGACT 856
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 360 GAGTCCCTTGCGCTCAGCTCAGAGTCAAGACCGGAGGCTCCCTGCTCCCGCTCAGAGACT 405
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 857 AGAATTTCCAGAGATAGAGATATCCAGAGTCCCGCTGCTGACGCTGGGCT 916
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 406 ---CTTCTCAGGGAATAGAGATATCCAGAGTCCCGCTGCTGCTGCTGCTGCTGCTGCT 461
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 917 TCTGCTGCTCCCTCCCAAGGATGCTGGTTCATTTAGAGTGTGACATCCAGCT 976
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 462 TCTGCTGCTCTTCTCCCATGCTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 977 GCTGCTGAGTGTCCCATGAGAGATGCAAGTGTGATTTCTGACTCTCTCTCTCAG 1036
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 520 GCTGAGAGAGTGTCCCATGAGAGATGCAAAATGCTGATGCTGCTGCTGCTGCTGCTGCTG 579
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: January 31, 2003, 02:21:31  
Job time : 175 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:01:58 ; Search time 3060 Seconds  
(without alignments)  
12924.634 Million cell updates/sec

Title: US-09-622-846-16  
Perfect score: 2442  
Sequence: 1 tactcccgagctcgcgggtc.....tgcctatgccttccttgg 2442

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estlin.\*  
4: em\_estlun.\*  
5: em\_estlov.\*  
6: em\_estlpl.\*  
7: em\_estro.\*  
8: em\_hlc.\*  
9: gp\_estl.\*  
10: gp\_estl2.\*  
11: gb\_hlc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inu.\*  
20: em\_gss\_dln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rtd.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	548.2	22.4	963	13	BM475710	AGENCOURT
2	481.8	19.7	1042	12	BF797314	602256935
3	476	19.5	676	10	AV730970	AV730970
4	474	19.4	673	12	BF739367	BF739367
5	467	19.1	698	10	AV730652	AV730652
6	450.8	18.5	637	9	AL602989	DXFZP086J

7	443.6	18.2	953	9	AL538335	AL538335
8	437	17.9	950	14	BO711975 <td>BO711975 </td>	BO711975
9	435.2	17.6	992	14	BO710264 <td>BO710264 </td>	BO710264
10	405.6	16.6	732	10	AV695124 <td>AV695124 </td>	AV695124
11	398.8	16.3	655	17	AG094772 <td>AG094772 </td>	AG094772
12	395.2	16.2	713	17	AG119067 <td>AG119067 </td>	AG119067
13	394.2	15.8	742	10	AV694018 <td>AV694018 </td>	AV694018
14	385	15.7	1027	9	AL567261 <td>AL567261 </td>	AL567261
15	382.4	15.7	731	12	BS48958 <td>BS48958 </td>	BS48958
16	382.2	15.7	1018	17	AF057114 <td>AF057114 </td>	AF057114
17	371	15.2	822	9	AL519039 <td>AL519039 </td>	AL519039
18	350.4	14.3	463	12	BF873745 <td>BF873745 </td>	BF873745
19	350.4	14.3	674	14	BO328156 <td>BO328156 </td>	BO328156
20	349	14.3	467	14	BM694948 <td>BM694948 </td>	BM694948
21	345.6	14.2	605	14	BO328128 <td>BO328128 </td>	BO328128
22	338.6	13.9	499	12	BF871243 <td>BF871243 </td>	BF871243
23	336	13.8	450	10	AM819527 <td>AM819527 </td>	AM819527
24	334	13.7	494	12	BF737104 <td>BF737104 </td>	BF737104
25	320.4	13.1	479	10	AM847815 <td>AM847815 </td>	AM847815
26	319.4	13.1	536	10	AM603938 <td>AM603938 </td>	AM603938
27	319.4	13.1	663	17	AC039086 <td>AC039086 </td>	AC039086
28	312.4	12.8	382	13	BI031182 <td>BI031182 </td>	BI031182
29	309.4	12.7	574	14	W60762 <td>W60762 </td>	W60762
30	308.4	12.6	1032	14	BO706969 <td>BO706969 </td>	BO706969
31	306.6	12.5	472	12	BF902064 <td>BF902064 </td>	BF902064
32	305.2	12.5	555	12	BF953853 <td>BF953853 </td>	BF953853
33	299.8	12.3	1101	12	BE869028 <td>BE869028 </td>	BE869028
34	295.2	12.1	918	9	AL542545 <td>AL542545 </td>	AL542545
35	294	12.0	539	12	BF848790 <td>BF848790 </td>	BF848790
36	291.6	11.9	512	14	BO328194 <td>BO328194 </td>	BO328194
37	291.2	11.9	617	10	AM206422 <td>AM206422 </td>	AM206422
38	288.8	11.8	719	14	BO016844 <td>BO016844 </td>	BO016844
39	283.8	11.6	429	10	AV696063 <td>AV696063 </td>	AV696063
40	282.4	11.6	487	14	BO300975 <td>BO300975 </td>	BO300975
41	281	11.5	491	10	AV732289 <td>AV732289 </td>	AV732289
42	277.2	11.4	431	10	BE165654 <td>BE165654 </td>	BE165654
43	276.8	11.3	845	9	AL542095 <td>AL542095 </td>	AL542095
44	276.8	11.3	890	9	AL541086 <td>AL541086 </td>	AL541086
45	276	11.3	635	13	BG974623	BG974623

## ALIGNMENTS

RESULT 1  
LOCUS BM475710 963 bp mRNA linear EST 05-FEB-2002  
DEFINITION AGENCOURT\_6480189 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:5575764  
5', mRNA sequence.  
ACCESSION BM475710  
VERSION BM475710.1 GI:18524752  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Carnivora; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 963)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LLM12326 row: 1 column: 13  
High quality sequence stop: 716.  
Location/Qualifiers  
1. 963

## FEATURES

source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5575764"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: testis; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

```

```

BASE COUNT      203 a      270 c      279 g      211 t
ORIGIN
Query Match      22.4%; Score 548.2; DB 13; Length 963;
Best Local Similarity 85.0%; Pred. No. 4.7e-131;
Matches 718; Conservative 0; Mismatches 118; Indels 9; Gaps 9;

```

```

OY 182 ATGATGGGCGGCGACCTGGGCTGCGACGGGCGCTCTCCGGGATAGACATATGCC 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 ATGATGGGCTGCGACCTGGGCTGGAAGGGCGCTCTCCGGGATAGACATAGCGCC 62
OY 242 TAGCATGCAAGGATTAACCTCGCCCTGAACGAGACCTCGCTCTGACCGCAGCGAC 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 AACGATGCAAGGATTAACATAGCCCGGAACTAGACCTCGCTCTGACCGCGCGGAC 122
OY 302 ACTGCGGCTAGATCTCCAGGCGGAGTGTGAGGCGCAATGTGCTGACAAAGAGAA 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 ATGCGGCTGAGATCACCAAGCGGAGGCGGAGGCGGAAATTTGACAGCATGACG 182
OY 362 GCGTACCTGAGGCGACGTCGTGAGTGGCTTCACAGATACCTGAGAACGGGAGAG 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 GCGTACCTGAGGCGACGTCGTGAGAGAGCT-CGACAGACCTGAGAACGGGAGAG 241
OY 422 ATGCTGAGGCGGCGGCTGACAGGCGGCGCTCCCTGATCTCTGATACGCTC 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 AGCGTGAAGCTCACGGGTACAGGAGAACACAGACCGCTCTCGATGCGCTGATGTC 301
OY 482 TCACGCTGGGCTGACACAGAGAGAGAGGAAATGGGACCAACACTAGATATCGCCCTC 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CTGGGCTGGGCTGCCACAAAGAGAGAAATGGGACCAACACTAGATATCGCTCTC 361
OY 542 CCTGTGCTCTGAGGAGAGAGGATCTCTCGGCTTCGAGATCTGTACCAAGAGTAT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TCTGTGCTCTGAGGAGAGAGGATCTCTCGGCTTCGAGATCTGTACCAAGAGTAT 421
OY 602 TCTGAGGCGGCTGCTCTCTGAGCAATTAAGGAGTAAAGTCTCTGAGGAGTGA 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 TCTGAGGCTGCGGCTGCTCTCTGATNCAATTAAGGAGTAAATCTCTGAGGAGTGA 480
OY 662 GGGAGAGCAATCCCTGGAAGACATGATGAGGGTTCCTTTGACCCCA-CAGCAGCTT-G 719
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GGGAGAGCAATCCCTGGAATATGATGAGGGTTCCTTTGACCCCAAGAGAGCTTGC 540
OY 720 GCACAGAGACTTTCCTCAGGCTGTTCTCTGCTCCTACACATCATGTGTGTGGGGT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GCGCCGTTACTTTCCCTCAGGCTGTTCTCTGCTTACACTCAATGTGTGTGGGGT 600
OY 780 CTGACTCCAGCTCTCTGATGCTCTGCTGCTCTGCTCCTACAGTCAAGAGAGTCCCTGC 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CTGAGTCCAGCTCTCTGATGCTCTCAGCTCCACACAGTCAAGAGTCAAGTCACTGT 660
OY 840 TCCGCGCTGAGAGACTTTCCTCAAGGAA-TAGGAGATTAATCCAGGCGGCTGCT 898
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 TCCGCTC-CTGAGGAGAGTGTGATTTCCAGGAAATTCGAGATTAATCCAGTATCTGT 719
OY 899 CAGGCTGTGT-GTCTGGGTTCTGTGCTCTCTCCCTCCACAGGAGTAT-CTGTTCAATCT 956
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 720 CAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
OY 957 TAGGATGTACATCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1016
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 780 CAGGATGCGCAATATG-CGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 838

```

```

OY 1017 TTTCT 1021
    ||| |
Db 839 TTTT 843

```

```

RESULT 2
BF797314 1042 bp mRNA linear EST 12-JAN-2001
LOCUS
DEFINITION
602256935F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:434036 5',
mRNA sequence.
ACCESSION
BF797314.1 GI:12102368
VERSION
BF797314
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
1 (bases 1 to 1042)
NIH-MGC http://mgi.mcg.mcg.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: L1AM9952 row: e column: 09
High quality sequence stop: 703.

```

```

FEATURES
source
Location/Qualifiers
1..1042
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:434036"
/clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: lymph; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.86 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

```

```

BASE COUNT      252 a      285 c      306 g      189 t
ORIGIN
Query Match      19.7%; Score 481.8; DB 12; Length 1042;
Best Local Similarity 83.9%; Pred. No. 8.2e-114;
Matches 627; Conservative 0; Mismatches 112; Indels 8; Gaps 7;

```

```

OY 290 ACCGACGAGACACTGCGGCTGATCTCCAGCGCAATGTGAGGCGGCAATGTGCT 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ACCGCGCGGACATGCGGCTGATCTCCAGCGCAATGTGAGGCGGCAATGTGCTCA 60
OY 350 GAACAAGAGAGACCTACTCTGAGGAGGACGCTGTGAGTGTGCTCCAGATCTGAG 409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GAGGAGATCGAGGCTTACCTGAGGAGGACGCTGTGAGAGGCT-CGACACACTGAG 119
OY 410 AACGGAGAGAGATGCTGAGCGCGGCTTACAGGAGGAGTGGGCGCTCTGATCT 469
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 AACGGAGAGAGAGCTGAGCTGACGCTTACAGGAGGAGGAGGAGGAGGAGGAGG 179
OY 470 CTTGAGACTCTGACGCTGCGCTAGCACAAGAGAGAGGAGGAGGAGGAGGAGGAG 529
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 CTTGAGACTCTGCGCTGCGCTTCCACAAAGAGAGGAGGAGGAGGAGGAGGAGGAG 239
OY 530 AATATGCGGCTCTGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 AATGTGCTCTCTGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 299

```

[illegible]







```

/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/Note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      191 a      262 c      301 g      198 t      1 others
ORIGIN

Query Match      18.2%; Score 443.6; DB 9; Length 953;
Best Local Similarity 75.3%; Pred. No. 6.4e-104;
Matches 706; Conservative 1; Mismatches 95; Indels 136; Gaps 7;

QY 1034 CAGACCCCCCAGACACAGCTGACCCACCTCTCTTTGACTGAGGCCACCTCTGA 1093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 CGAGCGCCCCAAGACGATATGATACACGCTCTCTGACCAWAGGCCACCTCTGA 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1094 GGTGCTGGGCGCTGGGCTTACCTGCGAGATCATACTGACCTGCGAGCGGATGGG 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 GGTGCTGGGCGCTGGGCTTACCTGCGAGATCATACTGACCTGCGAGCGGATGGG 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1154 AGACACGACCCAGACAGCTGAGTGTGAGACGAGCCCTGAGGGATGACACCTTCC 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AGGACACGACCCAGACAGCTGAGTGTGAGACGAGCCCTGAGGGATGACACCTTCC 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1214 AGAGTGGGAGCTGTGTGCTCTCTGAGAGAGAGAGATACAGTGCATGTC 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 AGAGTGGGAGCTGTGTGCTCTCTGAGAGAGAGAGATACAGTGCATGTC 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1274 AGCATGAGGGGCTGCGGAGACCCCTCATGCTGATGAGATGAGAGGATGAGGCA 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 AGCATGAGGGGCTGCGGAGACCCCTCATGCTGATGAGATGAGAGGATGAGGCA 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1334 TCATGCTGTGATGAGGAGAGAGAGCTCTGTAAGACCTTTAAGAGGTCGATGAG 1393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 ----- 424

QY 1394 GCGTGGGGGTGACAGACCTTACCTCTTCCAGAGCACTTCCCTGCGCAC 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 ----- 424

QY 1454 CATCCCATCATGAGGATGCTGTGCTGAGCTGTGCTGCTGAGTCACTGAGAC 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 CATCCCATCATGAGGATGCTGTGCTGAGCTGTGCTGAGTCACTGAGAC 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1514 TCGGCTGCTGCTGCTGCTGAGAGAGAGCTGAGTAAAG -AAGGGGTGACAGTG 1572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 TCGTGTGCTGCTGCTGCTGAGAGAGAGCTGAGTAAAG -AAGGGGTGACAGTG 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1573 GGGTCTAGTTTCTTGTCCATCGGGGCTTCAAGCCCAAGTAGAAGTGTGCTGCG 1632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 GGGTCTAGTTTCTTGTCTCACTGAGGCTTCCAGACCCAGTAGAAGTGTGCTGCG 624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1633 TGTGTACTGGAGACACATTCACATCATGAGCTGAGCTGAGCTGCTGTGCGCA 1692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 625 TGTGTACTGGAGACACATTCACATCATGAGCTGAGCTGAGCTGCTGTGCGCA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1693 GCACCTTCTCTTTTGTAAACACACTGTGACATGAGAGAGATTAATACCTGTATG 1752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 685 GCACCTTCTCTTTTGTAAACACACTGTTAATTAAGAGAGATTAATACCTGTATG 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1753 TGTAGTATGAGGAGACCTGATCCAGTAATCAAGGT -GAGGAGAAGTCTCTGCTGA 1810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 GGGGCTGAT -GGGAGCTGATCCAGAGTCAACAAGTCAAGGAGGAGGCTCTCTCT 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1811 GACGACCTTAAGAGGAGCACTGTGTGAGAGACCCACATCTGCTTCTTCTTCTCTGA 1870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 797 GAGGACCTTCAGAGGCGGCTGTGTCAGACCCACACCTGCTTCTTCATCTTCTGA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1871 T--CGCCCTGGGCTGAGACACATTTCTGSAACCTCTGAGGTCACAGACTAGA 1928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 857 TCCGCGCCTGGGCTGAGTCACACATTTCTGSAACCTCTCTGAGGTCACAGACTAGA 916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1929 GGTTCCTCTAGGACCTCAGGCGCCCTCCACCTTCTG 1966
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 917 GGTTCCTCTAGGACCTCAGGCGCCCTCCACCTTCTG 953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
BQ711975      950 bp      mRNA      linear      EST 16-JUL-2002
LOCUS
DEFINITION
AGENCOURT_7975897 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214729
5', mRNA sequence.
ACCESSION
BQ711975
VERSION
BQ711975.1 GI:21850874
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 950)
NIH-MGC http://mgi.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
UNPUBLISHED (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLM at:
http://lmage.llnl.gov
Plate: LCM2382 row: 1 column: 02
High quality sequence stop: 571.
Location/Qualifiers
1..950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6214729"
/clone_11b="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: spleen; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
NIH_MGC Library."

BASE COUNT      192 a      278 c      257 g      223 t
ORIGIN

Query Match      17.9%; Score 437; DB 14; Length 950;
Best Local Similarity 80.4%; Pred. No. 3.3e-102;
Matches 589; Conservative 0; Mismatches 130; Indels 14; Gaps 6;

QY 1434 GAGCAGTCTTCCGCCACACATCCCATCATGATGCTGCTGCTGCTGCTCT 1493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 GAGCAGTCTTCCGCCACACATCCCATCATGATGCTGCTGCTGCTGCTCT 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1494 GCACCTTAATCTGAGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 GGAAGCTGTATCTGAGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1554 AAGGAGGGGTGAGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 GGGAGAGGATGA -AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,  
1 (bases 1 to 732)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
TITLE  
JOURNAL  
MEDLINE  
COMMENT  
Contact: Zenguan Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhanjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.  
FEATURES  
Source  
1. 732  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GKASD09"  
/clone="GKASD09"  
/tissue\_type="hepatocellular carcinoma"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI"  
BASE COUNT 141 a 185 c 197 g 205 t 4 others  
ORIGIN  
Query Match 16.6%; Score 405.6; DB 10; Length 732;  
Best Local Similarity 78.9%; Pred. No. 4.2e-94;  
Matches 624; Conservative 0; Mismatches 92; Indels 75; Gaps 9;  
QY 1579 GAGTTTCTGTCACGCGGGGTTTCAGCCGAGGTACAGTGGCCCTGGCTGTTA 1638  
DB 1 GAGATTTCTTGTCTACTGAGGGTTCCAGACCCAGGTGAGTGGCTGCTGTTA 60  
QY 1639 CTGGAGACACCATCACCACCTACCTGAGCCCTGCTGTCAGACACT 1698  
DB 61 CTGGAGACACCATCACAATATGAGGCTACCCAGCGCTGCTGTCAGACACT 120  
QY 1699 TCTCTTTGTAAGACACCTGACATGAGAGAGATTTATGATGATGTTAGT 1758  
DB 121 ACTCTTTGTAAGACACCTGTTTGAAGAGACATTTATGATGATGTTAGT 176  
QY 1739 GATGGGACCTGATCCAGTATGACAGGT--CAGGAGAAAGTCCCTGCTAAGACAGA 1816  
DB 177 GAT--GGGACCTGATCCAGTATGACAGGTGAGGAGGAGTCCCT-----GAGGAC 228  
QY 1817 CCTTAGGAGGAGGAGTGGTGCAGAGACCATCATCTGCTTCTGTTTTCCTGAT--CGC 1874  
DB 229 CTTCAGAGAGGCGGTGGTCCAGAGACCATCTGCTTCTGATGTTTTCCTGATCCGCC 288  
QY 1875 CCTGGGCTGACGTACACATTTCTGAAACTTCTGAGGCTCAAGACTAGAGGTTCC 1934  
DB 289 CCTGGGCTGACGTACACATTTCTGAAACTTCTGAGGCTCAAGACTAGAGGTTCC 348  
QY 1935 TCTAGACCTCAAGGCGCTGACCTTCTGAGGCTCAAGACTAGAGGTTCC 1994  
DB 349 TCTAGACCTCAAGGCGCTGAGGCTTCTGATGTTTCAAGAGACATTTCTTCCAGAG 408  
QY 1995 ATTGAAAGAGGAGGAGTCTCTCAAGGCTCAAGTAAAGTAAAGAGGCTGATCCCTGA 2054  
DB 409 ATGAGAA----- 415  
QY 2055 GATCCTGGAGATCTTGTGTTGGAG--CAATGGGAGGAGTCAACCCACCATATTCCTC 2113

DB 416 -ATCAGTGGAGATTTGTTGGAGCCGTTGGGAGCTACCCACCATATCTC 474  
QY 2114 CTCTGGCCACA--TCTCCTGTCCTGACAGAGGCTGTTTGTCTCTAGAGCAG 2172  
DB 475 CTCTAGCCACATCTCTGTGGATGTGACAGANTTGTGTTTGTCTACCCAGCAG 534  
QY 2173 TGACATGGCCAGGCGCTCAATGTTCTCTACAGCGCTGTAAGTCAACCCGGGGGG 2232  
DB 535 TGACAGTGGCCAGGCGCTCAATGTTCTCTACAGCGCTGTAAGTCAACCCGGGGGG 594  
QY 2233 CTGATGTTGTTGGGTTGTTGAGGGAACAGGAGCATATGCTGTAGAGGTTCTT 2292  
DB 595 CTGATGTTGTTGGGTTGTTGAGGGAACAGGAGCATATGCTGTAGAGGTTCTT 654  
QY 2293 GACTTCATGTTATGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 2352  
DB 655 GACTTCATGTTATGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 711  
QY 2353 TATGAAATTTGT 2363  
DB 712 TCCAAATTTGTT 722  
RESULT 11  
AG094772/C 655 bp DNA linear GSS 03-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-095K06.R, genomic survey sequence.  
DEFINITION AG094772  
ACCESSION AG094772.1 GI:1664574  
VERSION GSS.  
KEYWORDS Pan troglodytes male lymphoblast DNA, clone\_11b:PTB Chimpanzee Male  
SOURCE BAC library clone:PTB-095K06.R.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
REFERENCE  
1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoh,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 655)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoh,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpesgsc.riken.go.jp, URL:http://hqp.gsc.riken.go.jp/  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the Red process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
FEATURES  
Source  
1. 655  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-095K06.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_11b="PTB Chimpanzee Male BAC library"  
BASE COUNT 167 a 184 c 154 g 149 t 1 others  
ORIGIN  
Query Match 16.3%; Score 398.8; DB 17; Length 655;  
Best Local Similarity 84.4%; Pred. No. 2.3e-92;  
Matches 508; Conservative 0; Mismatches 87; Indels 7; Gaps 5;



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 742)  
 Xiu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
 Xiao, H., Ou, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
 Hu, G., Gu, J., Chen, Z., and Han, Z.  
 Insight into hepatocellular carcinogenesis at transcriptome level  
 by comparing gene expression profiles of hepatocellular carcinoma  
 with those of corresponding noncancerous liver  
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 21625106  
 JOURNAL  
 MEDLINE  
 COMMENT  
 Contact: Zenguan Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@cnhg.sh.cn  
 This clone is available at CHGC in Shanghai.  
 Location/Qualifiers  
 1. 742  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="GKC"  
 /tissue\_type="hepatocellular carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="SOLR"  
 /note="Vector: Bluescript sk(-); Site\_1: EcoRI; Site\_2:  
 XhoI"  
 BASE COUNT 144 a 185 c 198 g 209 t 6 others  
 ORIGIN  
 Query Match 16.1%; Score 394.2; DB 10; Length 742;  
 Best Local Similarity 78.7%; Pred. No. 3,8e-91;  
 Matches 635; Conservative 0; Mismatches 94; Indels 78; Gaps 11;  
 Oy 1579 GAGTTTCTTGTCCAGTGGGGTTTCAAGCCAGGTAGAACTGGCCCTGGCTTGA 1638  
 1 GAGATTTCGTCTCAGTGAAGGTTCCAGACACCCAGGTAAAGTGGCCCTGGCTTGA 60  
 Oy 1639 CTGGAGACACCATTCACACTGATGGGCTTACCAGGCTTGGCCCTGGTGCACACCT 1698  
 61 CTGGAGACACCATTCACAAATTAAGGCTTACCAGGCTTGGCCCTGGTGCACACCT 120  
 Oy 1699 TCTCTTTGTAAGACACCTGTGACAAATGAAGAGACAGATTATTCCTGATGTTAGT 1758  
 121 ACTCTTTGTAAGACACCTGTG---TTGAAGAGACAGATTATTCACCTGTATATGGCGGT 176  
 Oy 1759 GATGGGGACCGATCCAGTAATACAGGT--CAGAGAGAGGTCCCTGGCTAAGAGACAGA 1816  
 177 GAT--GGGACCGATCCAGTCCAGTCAAGTACAGGGGAAAGTCCCT-----GAGGAC 228  
 Oy 1817 CCTTGAAGGGACAGTGGTGGAGAGCCACATCTGCTTCTCTTCTTCTTCTGAT--CGC 1874  
 229 CTTCAGAGGGCGGTTGGTCCAGGACCCACACCTGCTTCTTCTTCTTCTGATCCGCC 288  
 Oy 1875 CCTGGGTGTGAGTACACATTTCTGGAACCTTCTGAGGCTCCAGACTAGAGAGTTC 1934  
 289 CCTGGGTGTGAGTACACATTTCTGGAACCTTCTGAGGCTCCAGACTAGAGTTC 348  
 Oy 1935 TCTAGACCTCATGAGCCCTGACACCTTCTGAGCTTCTGACAGACATTTCTTCCACAG 1994  
 349 TCTAGACCTTAAGCCCTGAGCTTCTTCTGATATCTACAGACATTTCTTCCACAG 408  
 Oy 1995 ATTGAAGAGAGAGGACTCTGAGGCTGACAGTAAGTATGAAGAGAGCTGATCCCTGA 2054  
 409 ATAGGA----- 415  
 Oy 2055 GATCCCTGGAGATCTGTGTTGGAG--CATGGGAGAGTACACCCACCCACAAATTCCTC 2113  
 416 -ATCAGCTGGAGATCTGTGTTGGAG--CATGGGAGAGTACACCCACCCACAAATTCCTC 474

Oy 2114 CTCTGAGCCACATC-TCCTGTGTCCTGACAGGTGCTGTTTGTCTACTAGACAG 2172  
 475 CTCTAGCCACATCTTCTGTGGATCTACAGAGTTCGTTTGTCTACCCAGGAG 534  
 Oy 2173 TGACAGTCCAGGAGCTTAATGTCTCTCAGGCTGTAAAGTGACACCCGGGGG 2232  
 535 TGACAGTCCAGGAGCTTGAATGTCTCTCAGGCTGTAAAGTGACAGCTGAGAGG 594  
 Oy 2233 CCGATGTGTG--TGAGTTGTGAAGGAGACAGGAGACATAGCTGTCTAT--GAGTTTC 2289  
 595 CCGATGTGTGTGTGGTGTGGCCGAGACAGTGCAGCTGTCTATGGGGGTTTC 654  
 Oy 2290 TTTGACCTCAATGATATGAGCATGTGATGGCTGTTTAAAGTGCACCCCTGAC 2349  
 655 TTTGACATGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711  
 Oy 2350 TGATATGATTTGTTGATATATTTT 2376  
 712 AGATACGAATNTGTCATGATATTTT 738  
 RESULT 14  
 AL567261/c 1027 bp mRNA linear EST 16-FEB-2001  
 LOCUS  
 DEFINITION AL567261 LTI\_FL013\_Fbrn1 Homo sapiens CDNA clone CS0DF027YA18 3  
 prime, mRNA sequence.  
 ACCESSION AL567261  
 VERSION AL567261.1 GI:12920442  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 1027)  
 Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 Location/Qualifiers  
 1. 1027  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="CS0DF027YA18"  
 /dev\_stage="LTI\_FL013\_Fbrn1"  
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand  
 cDNA was primed with a NotI-Oligo(dT) primer. Five prime  
 end enriched, double-stranded cDNA was digested with Not I  
 and cloned into the Not I and Eco RV sites of the  
 pCMVSPORT 6 vector. Library was constructed by life  
 technologies. Contact : Feng Liang Life technologies, a  
 division of Invitrogen 9800 Medical Center Drive Rockville  
 Maryland 20850, USA fax : (1) 301 610 8371 Email :  
 fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
 BASE COUNT 276 a 263 c 266 g 218 t 4 others  
 ORIGIN  
 Query Match 15.8%; Score 385; DB 9; Length 1027;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-88;  
 Matches 493; Conservative 1; Mismatches 76; Indels 13; Gaps 5;  
 Oy 1453 CCAATCCCATCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1512  
 1027 CCAATCCCATCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968  
 Oy 1513 CTGGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1571







GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 20:57:28 (Search time 470 Seconds  
(without alignments)  
11700.808 Million cell updates/sec)

Title: US-09-622-846-16

Perfect score: 2442  
Sequence: 1 tactccgagctccggtc.....ttgtcatgcttccttcttg 2442

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :  
N.Geneseq\_101002:\*  
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2442	100.0	2442	20	AA225755 Human HLA-G gene I
2	2440.4	99.9	2442	20	AA225756 Human HLA-G gene I
3	2420	99.1	2441	20	AA225757 Human HLA-G gene D
4	2416.8	99.0	2441	20	AA225758 Human HLA-G gene D
5	2395.4	98.1	148834	24	ABR83570 Human cDNA differe
6	1829	74.9	4003	24	ABR84085 Human cDNA differe
7	1554	63.6	3098	22	ABR18125 Human nervous syst
8	1554	63.6	3098	22	AA540621 DNA encoding human
9	1554	63.6	3098	22	AA104024 Human reproductive

## ALIGNMENTS

10	1554	63.6	3098	22	AAK86871	Human immune/haema
11	1551.6	63.5	4316	22	ABR83122	HLA-Cw ovarian tum
12	1551.6	63.5	4316	24	ABN97218	Gene #3716 used to
13	1423	58.3	3357	22	AA163980	Human polynucleoti
14	1420.6	58.2	3372	22	AA163979	Human polynucleoti
15	1420.6	58.2	3372	22	AA164011	Human polynucleoti
16	1415	57.9	6553	18	AA161639	HLA B27 consensus
17	1407.4	57.6	3357	22	AA163981	Human polynucleoti
18	1336.6	54.7	3874	8	AA163978	Sequence of genom
19	1333.4	54.6	1892	22	AA163975	Human polynucleoti
20	938.6	38.4	4756	22	AA163974	Human polynucleoti
21	937	38.4	4756	22	AA163974	Human polynucleoti
22	792.6	32.5	6944	24	ABR34026	Human DNA for stag
23	725.2	29.7	6944	24	ABR34027	Human DNA for stag
24	461.2	18.9	466	22	ABR42058	Human breast cell
25	461.2	18.9	466	22	ABR42059	Human breast cell
26	461.2	18.9	466	22	ABR52479	Human foetal liver
27	461.2	18.9	466	22	ABR52480	Human foetal liver
28	461.2	18.9	466	22	ABR22271	Probe #737 for gen
29	461.2	18.9	466	22	ABR22272	Probe #738 for gen
30	461.2	18.9	466	22	AAK00746	Human brain expres
31	461.2	18.9	466	22	AAK00747	Human brain expres
32	461.2	18.9	466	22	AAK26198	Human bone marrow
33	461.2	18.9	466	22	AAK26199	Human bone marrow
34	461.2	18.9	466	22	AA110829	Probe #762 for gen
35	461.2	18.9	466	22	AA110830	Probe #763 for gen
36	461.2	18.9	466	22	AA132087	Probe #773 used to
37	461.2	18.9	466	22	AA132088	Probe #774 used to
38	461.2	18.9	466	22	AA100754	Probe #745 used to
39	461.2	18.9	466	22	AA100755	Probe #746 used to
40	461.2	18.9	466	24	ABR00784	Human genome-deriv
41	461.2	18.9	466	20	AA25743	Human HLA-G gene e
42	460	18.8	460	20	AA25744	Human HLA-G gene e
43	458.4	18.8	460	20	AA25744	Human HLA-G gene e
44	429.2	17.6	600	20	AAK8018	Histocompatibility
45	429.2	17.6	600	20	AAK38021	Histocompatibility

## RESULT 1

AA225755 standard; DNA: 2442 BP.

AA225755;

06-JAN-2000 (first entry)

Human HLA-G gene I-B8 and C-93 haplotype.

Human: HLA-G; pre-eclampsia; miscarriage susceptibility gene;

eclampsia; diagnosis; identification; pregnancy; miscarriage;

intrauterine growth retardation; infertility; autoimmune disease;

human leukocyte antigen-G; ss.

Synthetic.

Homo sapiens.

WO9943851-A1.

02-SEP-1999.

25-FEB-1999; 99WO-IE00012.

25-FEB-1998; 98IE-0000134.

12-AUG-1996; 98IE-0000668.

(UYNA-) UNITV NAT IRELAND CORK.

O'Brien M, Bermingham J, Quane KA, Jenkins DM, McCarthy TV;

WPI; 1999-590752/50.

XX Use of human leukocyte antigen-G (HLA-G), as a marker and in treatment  
 of abnormal pregnancy or infertility and autoimmune disease  
 XX  
 XX Disclosure: Page 68-69; 79pp; English.

XX The present invention describes the use of a human leukocyte antigen-G  
 (HLA-G) as a marker and in treatment for abnormal pregnancy or  
 CC infertility and autoimmune disease. Methods for the present invention  
 CC can be used for the diagnosis of susceptibility to, prevention or  
 CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,  
 CC miscarriage or miscarriage-related infertility. They can also be used  
 CC for treating autoimmune diseases. The present sequence represents a  
 CC HLA-G gene haplotype from the present invention.

XX Sequence 2442 BP: 485 A; 659 C; 735 G; 563 T; 0 other;

Query Match 100.0%; Score 2442; DB 20; Length 2442;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGTCTGGAGTCCACCCGAGCCCGGACCCCGCCAGACCTC 60  
 DB 1 TACTCCGAGTCTCCGGTCTGGAGTCCACCCGAGCCCGGACCCCGCCAGACCTC 60  
 QY 61 TACCTGGGAGAACCCCAAGGCGCTTACCAAAATCCCGGCGGTGGTCCGGCGAGG 120  
 DB 61 TACCTGGGAGAACCCCAAGGCGCTTACCAAAATCCCGGCGGTGGTCCGGCGAGG 120  
 QY 121 CGAGGCTCGTGGGCGGTGACCGAGGGGGTGGGCCAGTTTCACACCCCTCCAGTG 180  
 DB 121 CGAGGCTCGTGGGCGGTGACCGAGGGGGTGGGCCAGTTTCACACCCCTCCAGTG 180  
 QY 181 GATGATTTGGTGGCGAGTGGGGTCCGAGCGAGCTCTCCGGGGGATGAACAGTATG 240  
 DB 181 GATGATTTGGTGGCGAGTGGGGTCCGAGCGAGCTCTCCGGGGGATGAACAGTATG 240  
 QY 241 CTACGATGGCAAGATTACTCGCTGAAAGAGAGCTCGCTCTCGGACCGGACCGGA 300  
 DB 241 CTACGATGGCAAGATTACTCGCTGAAAGAGAGCTCGCTCTCGGACCGGACCGGA 300  
 QY 301 CACTCGGCTCAGATCTCCCAAGCGCAAGTGTGAGGGCGGCAATGGTGGTGAACAAGAG 360  
 DB 301 CACTCGGCTCAGATCTCCCAAGCGCAAGTGTGAGGGCGGCAATGGTGGTGAACAAGAG 360  
 QY 361 AGCTTACTGGAGGAGAGTGTGAGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 420  
 DB 361 AGCTTACTGGAGGAGAGTGTGAGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 420  
 QY 421 GATGCTGAGAGGCGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTAGACCT 480  
 DB 421 GATGCTGAGAGGCGGGTACCAAGGGGCAAGTGGGGCGCTCCCTGATCTCTAGACCT 480  
 QY 481 CTCACCTGCGCTAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 DB 481 CTCACCTGCGCTAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 QY 541 CCTCTGCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 DB 541 CCTCTGCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 601 TTTCTAGAGGCGGCT 660  
 DB 601 TTTCTAGAGGCGGCT 660  
 QY 661 GGGGAGAGCAATCCCTGAGAGAGATCAGGGGTTCCCTTGAAGAGAGAGAGAGAG 720  
 DB 661 GGGGAGAGCAATCCCTGAGAGAGATCAGGGGTTCCCTTGAAGAGAGAGAGAGAG 720  
 QY 721 CACCGAGAGCTTTCCCTCAGAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 DB 721 CACCGAGAGCTTTCCCTCAGAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 780

QY 781 TGAATCAGCTCTCTGAGATCCCTTGGCTCCGACCTGAGAGAGAGAGAGAGAGAG 840  
 DB 781 TGAATCAGCTCTCTGAGATCCCTTGGCTCCGACCTGAGAGAGAGAGAGAGAGAG 840  
 QY 841 CCCCCGAG 900  
 DB 841 CCCCCGAG 900  
 QY 901 AGCTGAGTCTGAG 960  
 DB 901 AGCTGAGTCTGAG 960  
 QY 961 ATGTCACATCCAGTGTCTGTGAGAGTCCATGAGAGAGAGAGAGAGAGAGAGAG 1020  
 DB 961 ATGTCACATCCAGTGTCTGTGAGAGTCCATGAGAGAGAGAGAGAGAGAGAGAG 1020  
 QY 1021 TGAATCAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 DB 1021 TGAATCAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 QY 1081 GAGGAG 1140  
 DB 1081 GAGGAG 1140  
 QY 1141 CAGGAG 1200  
 DB 1141 CAGGAG 1200  
 QY 1201 GATGAG 1260  
 DB 1201 GATGAG 1260  
 QY 1261 AGCTGAGTCTGAG 1320  
 DB 1261 AGCTGAGTCTGAG 1320  
 QY 1321 GAG 1380  
 DB 1321 GAG 1380  
 QY 1381 GAG 1440  
 DB 1381 GAG 1440  
 QY 1441 CTTCCTGAG 1500  
 DB 1441 CTTCCTGAG 1500  
 QY 1501 TACTCAG 1560  
 DB 1501 TACTCAG 1560  
 QY 1561 GGGGAG 1620  
 DB 1561 GGGGAG 1620  
 QY 1621 GGTGAG 1680  
 DB 1621 GGTGAG 1680  
 QY 1681 CCGTGTGAG 1740  
 DB 1681 CCGTGTGAG 1740  
 QY 1741 TACTCAG 1800  
 DB 1741 TACTCAG 1800  
 QY 1801 CCGTGTGAG 1860  
 DB 1801 CCGTGTGAG 1860  
 QY 1861 TTTTCTGATGAG 1920

|||||  
Db 1861 TTTTCCGTGATCGCCCGGTCTGCACTACACATTTTGGAATCTCGAGGGTCCAA 1920  
Qy 1921 GACAGAGAGGTTCCTTAGACCTCATGCGCCCTGACACCTTTCTGSCCTCTCACAGACA 1980  
Db 1921 GACAGAGAGGTTCCTTAGACCTCATGCGCCCTGACACCTTTCTGSCCTCTCACAGACA 1980  
Qy 1981 TTTTCTTCCACAGATTGAAAAGAGGAGGACTACTCTCAGAGCTGCAAGTAACTATGACAG 2040  
Db 1981 TTTTCTTCCACAGATTGAAAAGAGGAGGACTACTCTCAGAGCTGCAAGTAACTATGACAG 2040  
Qy 2041 AGGCTGATCCCTGAGATCTTTGGGATCTTGTGTTGGAGACCATGGGGAGGCTCACCCAC 2100  
Db 2041 AGGCTGATCCCTGAGATCTTTGGGATCTTGTGTTGGAGACCATGGGGAGGCTCACCCAC 2100  
Qy 2101 CCCACAATTCCTCCTCTGCGCACATCTCTGTGCTCTCTGACCAAGTGTCTTTTGTTC 2160  
Db 2101 CCCACAATTCCTCCTCTGCGCACATCTCTGTGCTCTCTGACCAAGTGTCTTTTGTTC 2160  
Qy 2161 TACTCTAGGACAGTACAGTCCCGCAGGGCTCTAATGTCTCTCTCAGGGCTTGTAAATGTA 2220  
Db 2161 TACTCTAGGACAGTACAGTCCCGCAGGGCTCTAATGTCTCTCTCAGGGCTTGTAAATGTA 2220  
Qy 2221 CACCCCGGGGGGCGGATGTGTGGGTTGTTGAGGGGAACAGGGGACATAGCTGTCTA 2280  
Db 2221 CACCCCGGGGGGCGGATGTGTGGGTTGTTGAGGGGAACAGGGGACATAGCTGTCTA 2280  
Qy 2281 TGAGCTTCTTGTGACTTCAATGTATGAGCATGTGATGGGCTGTTTAAAGTGTACCCCT 2340  
Db 2281 TGAGCTTCTTGTGACTTCAATGTATGAGCATGTGATGGGCTGTTTAAAGTGTACCCCT 2340  
Qy 2341 CACTGTGACTGATATGATTTGTCATGATATTTTCTGTAGTGAAGTACAGTGTGCT 2400  
Db 2341 CACTGTGACTGATATGATTTGTCATGATATTTTCTGTAGTGAAGTACAGTGTGCT 2400  
Qy 2401 GTGTGGAGTGTGAGCAAGATTTGTTCATGCTTCCCTTG 2442  
Db 2401 GTGTGGAGTGTGAGCAAGATTTGTTCATGCTTCCCTTG 2442

RESULT 2  
AA25756  
ID AA25756 standard; DNA; 2442 BP.  
XX  
AC AA25756;  
XX  
DT 06-JAN-2000 (first entry)  
XX  
DE Human HLA-G gene I-E8 and T-93 haplotype.  
XX  
KW Human: HLA-G; pre-eclampsia; miscarriage susceptibility gene;  
KW eclampsia; diagnosis; identification; pregnancy; miscarriage;  
KW intrauterine growth retardation; infertility; autoimmune disease;  
KW human leukocyte antigen-G; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN W09943851-A1.  
XX  
PD 02-SEP-1999.  
XX  
PF 25-FEB-1999; 99WO-IE00012.  
XX  
PR 25-FEB-1998; 98IE-0000134.  
XX  
PR 12-AUG-1998; 98IE-0000668.  
XX  
PA (UYNA-) UNIV NAT IRELAND CORK.  
XX  
PI O'Brien M, Beemingham J, Quane KA, Jenkins DM, McCarthy TV;  
XX  
DR WPI: 1999-590752/50.  
XX

PT Use of human leukocyte antigen-G (HLA-G), as a marker and in treatment  
PF of abnormal pregnancy or infertility and autoimmune disease  
PS Disclosure; Page 69-70; 79pp; English.  
XX  
XX The present invention describes the use of a human leukocyte antigen-G  
CC (HLA-G) as a marker and in treatment for abnormal pregnancy or  
CC infertility and autoimmune disease. Methods from the present invention  
CC can be used for the diagnosis of susceptibility to, prevention or  
CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,  
CC miscarriage or miscarriage-related infertility. They can also be used  
CC for treating autoimmune diseases. The present sequence represents a  
CC HLA-G gene haplotype from the present invention.  
XX  
XX Sequence 2442 BP; 485 A; 658 C; 735 G; 564 T; 0 other;  
Query Match 99.9%; Score 2440.4; DB 20; Length 2442;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TACTCCGAGTCTCCGGGTGAGATCCACCCGAGGCGCGGACCCGACCCCTC 60  
Db 1 TACTCCGAGTCTCCGGGTGAGATCCACCCGAGGCGCGGACCCGACCCCTC 60  
Qy 61 TACTCGGAGAAACCCCAAGCGCTTTACCAAAATCCCGGGGTGCTCCGGCGAGG 120  
Db 61 TACTCGGAGAAACCCCAAGCGCTTTACCAAAATCCCGGGGTGCTCCGGCGAGG 120  
Qy 121 CGAGGCTGGTGGGGGGGCGGACCGAGGGGCTGGGGCGAAGTCTACACCTCCAGT 180  
Db 121 CGAGGCTGGTGGGGGGGCGGACCGAGGGGCTGGGGCGAAGTCTACACCTCCAGT 180  
Qy 181 GATGATGGCTCGACCTGCGGCTGCGAGGAGCGCTCTCCGCGGATGTAACAGTATGC 240  
Db 181 GATGATGGCTCGACCTGCGGCTGCGAGGAGCGCTCTCCGCGGATGTAACAGTATGC 240  
Qy 241 CTACGATGGAAGATTAACCTCGCCCTTAACAGAGACCTGGCTCTCGAGCGGGA 300  
Db 241 CTACGATGGAAGATTAACCTCGCCCTTAACAGAGACCTGGCTCTCGAGCGGGA 300  
Qy 301 CACTGCGGCTCAGATCTCCAAAGCGCAAGTGTAGGCGGCAATGTGGTGAACAAAGAG 360  
Db 301 CACTGCGGCTCAGATCTCCAAAGCGCAAGTGTAGGCGGCAATGTGGTGAACAAAGAG 360  
Qy 361 AGCCTACCTGAGAGGACAGTGTGAGTGTCTCCAGATACCTGGAACGGGAAGA 420  
Db 361 AGCCTACCTGAGAGGACAGTGTGAGTGTCTCCAGATACCTGGAACGGGAAGA 420  
Qy 421 GATGCTGACAGCGCGGCTGACAGGGGAGTGGGCGCTCCGATCTCTGTAGACT 480  
Db 421 GATGCTGACAGCGCGGCTGACAGGGGAGTGGGCGCTCCGATCTCTGTAGACT 480  
Qy 481 CTCAGCTGCGCTTACGACAAAGAGAGAAATGGGACCAACATGAAATATCGCCT 540  
Db 481 CTCAGCTGCGCTTACGACAAAGAGAGAGAAATGGGACCAACATGAAATATCGCCT 540  
Qy 541 CCTCTGTGCTCTGAGGAGAGAGATCTCTGGTTTCCAGATCTCTGACAGAGAGTA 600  
Db 541 CCTCTGTGCTCTGAGGAGAGAGATCTCTGGTTTCCAGATCTCTGACAGAGAGTA 600  
Qy 601 TTTCTGAGGGCGCGCTGCTGCTGTGGACAATTAAGATGTAAGTCTGAGGGAGTGA 660  
Db 601 TTTCTGAGGGCGCGCTGCTGCTGTGGACAATTAAGATGTAAGTCTGAGGGAGTGA 660  
Qy 661 GGGGAAGACAATCCGGAAGACTGATCAGGGGTCTCTTGAACCCACAGCAGCTTGG 720  
Db 661 GGGGAAGACAATCCGGAAGACTGATCAGGGGTCTCTTGAACCCACAGCAGCTTGG 720  
Qy 721 CACGAGACTTTTCCCTCAGGCTGTCTGCTCTGCTTCACTCAATGTGTGGGGGTC 780  
Db 721 CACGAGACTTTTCCCTCAGGCTGTCTGCTCTGCTTCACTCAATGTGTGGGGGTC 780  
Qy 781 TGACTCCAGCTCTGTGATCTCTGCTTGGCTTCACATCAGGTGCAACCGAGGTCTCTGCT 840

Db 781 TGAATCCAGCTCCCTGAGTCCCTTGGCCCTCCAGTCCAGAGCCGAGGCTCCGCT 840  
 Oy 841 CCCCCGCTCAGAGACTAGAACTTCCAAAGAAATAGAGATATCCAGAGGCCCGCTGCC 900  
 Db 841 CCCCCGCTCAGAGACTAGAACTTCCAAAGAAATAGAGATATCCAGAGGCCCGCTGCC 900  
 Oy 901 AGGCTGCTGCTGAGGCTCTGCTGCTCCCTCCAGCCAGGATATGATTCATTTAG 960  
 Db 901 AGGCTGCTGCTGAGGCTCTGCTGCTCCCTCCAGCCAGGATATGATTCATTTAG 960  
 Oy 961 ATGCTCAGATCCAGGCTGCTGAGAGTGTCCATGAGAGATGCAAGTGTGATTTTC 1020  
 Db 961 ATGCTCAGATCCAGGCTGCTGAGAGTGTCCATGAGAGATGCAAGTGTGATTTTC 1020  
 Oy 1021 TGACTCTCTCTTTCAGAGCCGCCCAAGACACAGTGCACCCAGCCCTGCTTGCAT 1080  
 Db 1021 TGACTCTCTCTTTCAGAGCCGCCCAAGACACAGTGCACCCAGCCCTGCTTGCAT 1080  
 Oy 1081 GAGGCTCCTGAGGCTGCTGAGGCTGCTGCTTACCTGCTGAGATCATATGACCTGG 1140  
 Db 1081 GAGGCTCCTGAGGCTGCTGAGGCTGCTGCTTACCTGCTGAGATCATATGACCTGG 1140  
 Oy 1141 CAGGCGGATGGGAGGAGACACAGACCTGAGGCTGAGACCCAGGCTGCGAGG 1200  
 Db 1141 CAGGCGGATGGGAGGAGACACAGACCTGAGGCTGAGACCCAGGCTGCGAGG 1200  
 Oy 1201 GATGAACTTCCAGAAAGTGGGAGCTGTGTGTGCTTCTGAGAGAGACAGATATC 1260  
 Db 1201 GATGAACTTCCAGAAAGTGGGAGCTGTGTGTGCTTCTGAGAGAGACAGATATC 1260  
 Oy 1261 ACGTGCATGTGCAGCATGAGGAGGCTGCGAGGCTGCTGCTGAGATGAGAGAGAG 1320  
 Db 1261 ACGTGCATGTGCAGCATGAGGAGGCTGCGAGGCTGCTGCTGAGATGAGAGAGAG 1320  
 Oy 1321 GAGATGAGAGCATCATATGTCTGTAGGAGAAAGAGAGGCTCTCTAGAGACCTTTAAG 1380  
 Db 1321 GAGATGAGAGCATCATATGTCTGTAGGAGAAAGAGAGGCTCTCTAGAGACCTTTAAG 1380  
 Oy 1381 GGTGCTGCTGAGGCTGAGGCTGAGAGACCTTACCTTCTTCCAGAGCACT 1440  
 Db 1381 GGTGCTGCTGAGGCTGAGGCTGAGAGACCTTACCTTCTTCCAGAGCACT 1440  
 Oy 1441 CTTCCCTGCCACCACTCCCATCATGAGTATCGTGTGCTGCTGCTGCTGCTGCTG 1500  
 Db 1441 CTTCCCTGCCACCACTCCCATCATGAGTATCGTGTGCTGCTGCTGCTGCTGCTG 1500  
 Oy 1501 TAGTCACTGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 Db 1501 TAGTCACTGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 Oy 1561 GGGTGCAGAGTGGGCTGCTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 Db 1561 GGGTGCAGAGTGGGCTGCTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 Oy 1621 GTGTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 Db 1621 GTGTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 Oy 1681 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
 Db 1681 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
 Oy 1741 TACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 Db 1741 TACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 Oy 1801 CCTGCTTAAGAGACAGCTTAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 Db 1801 CCTGCTTAAGAGACAGCTTAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 Oy 1861 TTTTTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 Db 1861 TTTTTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920

Db 1861 TTTTTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 Oy 1921 GACTAGAGAGTCTCTAGAGACTCATGAGCCCTGAGCCCTTCTGCTGCTGCTGCTGCTG 1980  
 Db 1921 GACTAGAGAGTCTCTAGAGACTCATGAGCCCTGAGCCCTTCTGCTGCTGCTGCTGCTG 1980  
 Oy 1981 TTTTTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
 Db 1981 TTTTTCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
 Oy 2041 AGGCTGATCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
 Db 2041 AGGCTGATCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100  
 Oy 2101 CCGCAGATTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 Db 2101 CCGCAGATTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 Oy 2161 TACTCTAGGAGAGTACAGTCCAGAGGCTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220  
 Db 2161 TACTCTAGGAGAGTACAGTCCAGAGGCTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220  
 Oy 2221 CACCCGCGGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280  
 Db 2221 CACCCGCGGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280  
 Oy 2281 TGAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340  
 Db 2281 TGAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340  
 Oy 2341 CACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
 Db 2341 CACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
 Oy 2401 GTGTGAGCTGAGTGGCAGAGATTTGTCATGCTTCCCTTTG 2442  
 Db 2401 GTGTGAGCTGAGTGGCAGAGATTTGTCATGCTTCCCTTTG 2442  
 RESULT 3  
 AA225757  
 ID AA225757 standard; DNA; 2441 BP.  
 XX  
 AC AA225757;  
 XX  
 DT 06-JAN-2000 (first entry)  
 XX  
 DE Human HLA-G gene D-E8 and C-93 haplotype.  
 XX  
 KW Human; HLA-G; pre-eclampsia; miscarriage susceptibility gene;  
 KW eclampsia; diagnosis; identification; pregnancy; miscarriage;  
 KW intrauterine growth retardation; infertility; autoimmune disease;  
 KW human leukocyte antigen-G; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 PN MO9943851-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PF 25-FEB-1999; 99MO-IE00012.  
 XX  
 PR 25-FEB-1998; 98IE-0000134.  
 PR 12-AUG-1998; 98IE-0000668.  
 XX  
 PA (UYNA-) UNIV NAT IRELAND CORK.  
 XX  
 PI O'Brien M, Bermingham J, Quane KA, Jenkins DM, McCarthy TV;  
 DR WPI; 1999-590752/50.  
 XX  
 PT Use of human leukocyte antigen-G (HLA-G), as a marker and in treatment

PT of abnormal pregnancy or infertility and autoimmune disease -  
 XX Disclosure; Page 70-71: 79pp: English.

CC The present invention describes the use of a human leukocyte antigen-g  
 CC (HLA-G) as a marker and in treatment for abnormal pregnancy or  
 CC infertility and autoimmune disease. Methods from the present invention  
 CC can be used for the diagnosis of susceptibility to, prevention or  
 CC treatment of pre-eclampsia, eclampsia, intrauterine growth retardation,  
 CC miscarriage or miscarriage-related infertility. They can also be used  
 CC for treating autoimmune diseases. The present sequence represents a  
 CC HLA-G gene haplotype from the present invention.

XX Sequence 2441 BP: 488 A; 659 C; 735 G; 559 T; 0 other:

Query Match 99.1%; Score 2420; DB 20; Length 2441;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGGCTGGGATCCACCCGAGGCGCGGACCCGCGAGACCTC 60  
 DB 1 TACTCCGAGTCTCCGGGCTGGGATCCACCCGAGGCGCGGACCCGCGAGACCTC 60  
 QY 61 TACCTGGAGAGAACCCCAAGGCGCTTACCAAAATCCCGGGGTGGTCCGGGGAGGG 120  
 DB 61 TACCTGGAGAGAACCCCAAGGCGCTTACCAAAATCCCGGGGTGGTCCGGGGAGGG 120  
 QY 121 CGAGGCTGCTGGGCGGGGCTGACCGAGGGGGTGGGGCCAGGTTCTCACACCTCCAGTG 180  
 DB 121 CGAGGCTGCTGGGCGGGGCTGACCGAGGGGGTGGGGCCAGGTTCTCACACCTCCAGTG 180  
 QY 181 GATGATGGGCTGCGACCTGGGGTCCGACGAGACCTCTCCGGGGGTATGAACAGTATGC 240  
 DB 181 GATGATGGGCTGCGACCTGGGGTCCGACGAGACCTCTCCGGGGGTATGAACAGTATGC 240  
 QY 241 CTACAGATGGCAAGATTACTCTGCGCTGAAACGAGACCTCGCTCTGAGACCGCAGGA 300  
 DB 241 CTACAGATGGCAAGATTACTCTGCGCTGAAACGAGACCTCGCTCTGAGACCGCAGGA 300  
 QY 301 CACTCGGCTGAGATCTCCAAAGGCGAAGTGTGAGGGGGCCAAATGTGGTGAACAAAGAG 360  
 DB 301 CACTCGGCTGAGATCTCCAAAGGCGAAGTGTGAGGGGGCCAAATGTGGTGAACAAAGAG 360  
 QY 361 ACCCTACCTGAGGCGACGTCGTGAGTGGCTCCACAGATACCTTGAGAGACGGAGGA 420  
 DB 361 ACCCTACCTGAGGCGACGTCGTGAGTGGCTCCACAGATACCTTGAGAGACGGAGGA 420  
 QY 421 GATGCTGAGGCGCGGGGTACAGAGGGGAGTGGGGCCCTCGTGAATCTCTGTAGACT 480  
 DB 421 GATGCTGAGGCGCGGGGTACAGAGGGGAGTGGGGCCCTCGTGAATCTCTGTAGACT 480  
 QY 481 CTCACGCTGGCTAGCACAGAGAGAGAAAATGGGACCAACTAGATATCGCCCT 540  
 DB 481 CTCACGCTGGCTAGCACAGAGAGAGAAAATGGGACCAACTAGATATCGCCCT 540  
 QY 541 CCCTGTGCTCGAGGGGAGAGAAATCCCTCGGGTTCCAGATCTGTACAGAGAGTGA 600  
 DB 541 CCCTGTGCTCGAGGGGAGAGAAATCCCTCGGGTTCCAGATCTGTACAGAGAGTGA 600  
 QY 601 TTCTGAGGGCCGCTCTCTCTGAGCAATTAAGGATGAAGTCTTGAGGAGTGA 660  
 DB 601 TTCTGAGGGCCGCTCTCTCTGAGCAATTAAGGATGAAGTCTTGAGGAGTGA 660  
 QY 661 GGGGAGAGCAATCCCTGAGAGACATGATGAGGGGTCCCTTGAGCCGACAGAGCTTGG 720  
 DB 661 GGGGAGAGCAATCCCTGAGAGACATGATGAGGGGTCCCTTGAGCCGACAGAGCTTGG 720  
 QY 721 CACCAAGAGATTTTCCCTCAGGCTTGTCTCTGCTCAGACTCAATGTGTGTGGGGTTC 780  
 DB 721 CACCAAGAGATTTTCCCTCAGGCTTGTCTCTGCTCAGACTCAATGTGTGTGGGGTTC 780  
 QY 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGAGACGGAGGCTCCCTGCT 840  
 DB 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGAGACGGAGGCTCCCTGCT 840

DB 781 TGAGCTCAGCTCTCTGAGTCCCTTGGCTCAGTCAAGAGACGGAGGCTCCCTGCT 840  
 QY 841 CCCCGGCTGAGAGACTAGACTTTTCCAAAGATAGAGATTATCCAGAGTCCCGGTGTC 900  
 DB 841 CCCCGGCTGAGAGACTAGACTTTTCCAAAGATAGAGATTATCCAGAGTCCCGGTGTC 900  
 QY 901 AGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 DB 901 AGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 QY 961 ATGCTCAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 961 ATGCTCAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1021 TGAGCTCTCTTCCAGAGACCCGCGAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1080  
 DB 1021 TGAGCTCTCTTCCAGAGACCCGCGAGACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1080  
 QY 1081 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB 1081 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1141 CAGCGGATGGGAGAGACAGACCCAGAGAGTGGAGTGGAGAGACAGGCTGCGAGG 1200  
 DB 1141 CAGCGGATGGGAGAGACAGACCCAGAGAGTGGAGTGGAGAGACAGGCTGCGAGG 1200  
 QY 1201 GATGAGACCTTCCAGAAAGTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 DB 1201 GATGAGACCTTCCAGAAAGTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 QY 1261 AGCTGCTATGCTGAGATGAGGGGCTGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 DB 1261 AGCTGCTATGCTGAGATGAGGGGCTGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 QY 1321 GAGATGAGAGCATATGCTGTAGGAAAGAGAGACCTCTCTGAGACCTTTAAGCAG 1380  
 DB 1321 GAGATGAGAGCATATGCTGTAGGAAAGAGAGACCTCTCTGAGACCTTTAAGCAG 1380  
 QY 1381 GGTGCTGAGAGGGGTGGGGGTGAGAGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 DB 1381 GGTGCTGAGAGGGGTGGGGGTGAGAGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 QY 1441 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 DB 1441 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 QY 1501 TACTCACTGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 DB 1501 TACTCACTGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 QY 1561 GGGTGAAGAGTGGGGTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
 DB 1561 GGGTGAAGAGTGGGGTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
 QY 1621 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
 DB 1621 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
 QY 1681 CCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 DB 1681 CCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 QY 1741 TACCTGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 DB 1741 TACCTGATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 QY 1801 CTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
 DB 1801 CTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
 QY 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
 DB 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920





QY 841 CCCCCCTCAGAGACTAGAACTTTCCAGAGATAGAGATATCCAGAGTCCCGTTC 900  
 Db 841 CCCCCCTCAGAGACTAGAACTTTCCAGAGATAGAGATATCCAGAGTCCCGTTC 900  
 QY 901 AGGCTGGTGTGGGTCTGTCTCCCTCCACCCAGGTATCTGTTCAATTTAGG 960  
 Db 901 AGGCTGGTGTGGGTCTGTCTCCCTCCACCCAGGTATCTGTTCAATTTAGG 960  
 QY 961 ATGTGATCATCCAGAGTGGTGGAGTGGTCCATGAGATGAGAAAGTGGTGAATTTTC 1020  
 Db 961 ATGTGATCATCCAGAGTGGTGGAGTGGTCCATGAGATGAGAAAGTGGTGAATTTTC 1020  
 QY 1021 TGACCTCTCTTTCAGAACCCCTCCCAAGACACAGTGAACCACTGCTTTGACTAT 1080  
 Db 1021 TGACCTCTCTTTCAGAACCCCTCCCAAGACACAGTGAACCACTGCTTTGACTAT 1080  
 QY 1081 GAGGCAACCTGAGGTGGTGGGCTGCTGATCCCTGGGAGATCATAGACTGG 1140  
 Db 1081 GAGGCAACCTGAGGTGGTGGGCTGCTGATCCCTGGGAGATCATAGACTGG 1140  
 QY 1141 CACCGGATGGGAGGAGACCAAGACAGTGAAGTCTGAGAGACCAAGCTGACGG 1200  
 Db 1141 CACCGGATGGGAGGAGACCAAGACAGTGAAGTCTGAGAGACCAAGCTGACGG 1200  
 QY 1201 GATGGAACCTCCAGAGTGGGACCTGTGTGGTCTCTGAGAGAGAGACAGATAC 1260  
 Db 1201 GATGGAACCTCCAGAGTGGGACCTGTGTGGTCTCTGAGAGAGAGACAGATAC 1260  
 QY 1261 ACCTGCAATGTGAGCAGTGAAGGAGGCTGCTGAGTCTGAGAGAGAGAGAG 1320  
 Db 1261 ACCTGCAATGTGAGCAGTGAAGGAGGCTGCTGAGTCTGAGAGAGAGAGAG 1320  
 QY 1321 GAGGATGAGAGCATTCTGTCTGTAGGGAAGACAGACCTCTGGAAGACTTTAACAG 1380  
 Db 1321 GAGGATGAGAGCATTCTGTCTGTAGGGAAGACAGACCTCTGGAAGACTTTAACAG 1380  
 QY 1381 GGTGGTGTGAGAGGCTGGGGTCTCAGAGACCTTCACTTCACTCCCTCCAGAGCAGT 1440  
 Db 1381 GGTGGTGTGAGAGGCTGGGGTCTCAGAGACCTTCACTTCACTCCCTCCAGAGCAGT 1440  
 QY 1441 CTTCCTGCCCCACATCCCATCATAGGATATGCTGGGCTGTTTCAAGCCAGATGAA 1500  
 Db 1441 CTTCCTGCCCCACATCCCATCATAGGATATGCTGGGCTGTTTCAAGCCAGATGAA 1500  
 QY 1501 TAGTCACTGAGAGTGGGCTGCTGCTGTGAGGAAAGAGAGTCAAGTAAAGAG 1560  
 Db 1501 TAGTCACTGAGAGTGGGCTGCTGCTGTGAGGAAAGAGAGTCAAGTAAAGAG 1560  
 QY 1561 GGGTGAAGAGTGGGCTGCTGCTGTGAGGAAAGAGAGTCAAGTAAAGAG 1620  
 Db 1561 GGGTGAAGAGTGGGCTGCTGCTGTGAGGAAAGAGAGTCAAGTAAAGAG 1620  
 QY 1621 GGTGGCCTGCTGCTGTGAGGAAAGAGTCAAGTAAAGAGTCAAGTAAAGAG 1680  
 Db 1621 GGTGGCCTGCTGCTGTGAGGAAAGAGTCAAGTAAAGAGTCAAGTAAAGAG 1680  
 QY 1681 CCTGTGTGAGAGTGGGCTGCTGCTGTGAGGAAAGAGTCAAGTAAAGAG 1740  
 Db 1681 CCTGTGTGAGAGTGGGCTGCTGCTGTGAGGAAAGAGTCAAGTAAAGAG 1740  
 QY 1741 TACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 Db 1741 TACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
 QY 1801 CTTGGCTAAGAGACATTTAGAGAGGAGTGGTGAAGAGACCAATCTCTTTCTTG 1860  
 Db 1801 CTTGGCTAAGAGACATTTAGAGAGGAGTGGTGAAGAGACCAATCTCTTTCTTG 1860  
 QY 1861 TTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920  
 Db 1861 TTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920

QY 1921 GACTAGAGAGTCTCTAGAGACCTCATAGGACCTGACACCTTTCTGGCTCTACAGACA 1980  
 Db 1921 GACTAGAGAGTCTCTAGAGACCTCATAGGACCTGACACCTTTCTGGCTCTACAGACA 1980  
 QY 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGCTACTCTCAGGCTGCAGATAGTATGAAG 2040  
 Db 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGCTACTCTCAGGCTGCAGATAGTATGAAG 2040  
 QY 2041 AGGCTGATCCCTGATGATCTTGGAGATCTGTGTTGGAGCATGGGAGAGCTACCCAC 2100  
 Db 2041 AGGCTGATCCCTGATGATCTTGGAGATCTGTGTTGGAGCATGGGAGAGCTACCCAC 2100  
 QY 2101 CCAACATTTCTCTCTGAGGACCAATCTCTGCTGTCTGACCAAGAGTCTTTTCTTC 2160  
 Db 2101 CCAACATTTCTCTCTGAGGACCAATCTCTGCTGTCTGACCAAGAGTCTTTTCTTC 2160  
 QY 2161 TACTGTAGGAGTACAGTGGGAGGCTGATGATGATGATGATGATGATGATGATGAT 2220  
 Db 2161 TACTGTAGGAGTACAGTGGGAGGCTGATGATGATGATGATGATGATGATGATGAT 2220  
 QY 2221 CACCCCGGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
 Db 2221 CACCCCGGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
 QY 2281 TGAGGTTCTTGTGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
 Db 2281 TGAGGTTCTTGTGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2340  
 QY 2341 CACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
 Db 2341 CACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
 QY 2401 GTTGGGAGTGGTGGGAG 2420  
 Db 2401 GTTGGGAGTGGTGGGAG 2420

RESULT 5  
 ABRK3570/C  
 ID ABRK3570 standard; cDNA; 148834 BP.  
 XX  
 AC ABRK3570;  
 XX  
 DT 14-AUG-2002 (first entry)  
 XX  
 DE Human cDNA differentially expressed in granulocytic cells #141.  
 XX  
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; peridontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.  
 KW  
 OS Homo sapiens.  
 XX  
 PN W0200228999-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001W0-US30821.  
 XX  
 PR 03-OCT-2000; 2000US-237189P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 XX WPI: 2002-435328/46.  
 DR  
 XX  
 PT Detecting granulocyte activation by detecting differential expression



PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity

PS Claim 1; SEQ ID No 141; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating GA; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammation injury, Crohn's disease, ulcerative colitis,  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 148834 BP: 38942 A: 33672 C: 34501 G: 41719 T: 0 other:

Query Match 98.1%; Score 2395.4; DB 24; Length 148834;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2419; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 1 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGACCGCCAGACCTC 60  
 Db 12138 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGACCGCCAGACCTC 12079  
 QY 61 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGACCGCCAGACCTC 120  
 Db 12078 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGGACCGCCAGACCTC 12019  
 QY 121 CGAGGCTGCGTGGGCGGCGTGCACGAGGCGGCGGAGGTCTTCACACCTCCAGATG 180  
 Db 12018 CGAGGCTGCGTGGGCGGCGTGCACGAGGCGGCGGAGGTCTTCACACCTCCAGATG 11559  
 QY 181 GATGATGCTGCGTGGGCGGCGTGCACGAGGCGGCGGAGGTCTTCACACCTCCAGATG 240  
 Db 11958 GATGATGCTGCGTGGGCGGCGTGCACGAGGCGGCGGAGGTCTTCACACCTCCAGATG 11899  
 QY 241 CTAGGATGCGGAGGATTTACCTCGCTGGAAGGAGACCTGCTCTCGGCGGATGACAGTATGC 300  
 Db 11898 CTAGGATGCGGAGGATTTACCTCGCTGGAAGGAGACCTGCTCTCGGCGGATGACAGTATGC 11839  
 QY 301 CACTGCGGCTCAAGTCTCAAGGCGAAGTGTGAGCGCGCAATGTGTCTGACCAAGAGAG 360  
 Db 11838 CACTGCGGCTCAAGTCTCAAGGCGAAGTGTGAGCGCGCAATGTGTCTGACCAAGAGAG 11779

QY 361 AGCCTACCTGGAGGCGACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAGGAGAGCA 420  
 Db 11778 AGCCTACCTGGAGGCGACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAGGAGAGCA 11719  
 QY 421 GATGCTGACGCGCGGGGTACAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 480  
 Db 11718 GATGCTGACGCGCGGGGTACAGGGGAGTGGGGCGCTCCCTGATCTCTGTAGACCT 11659  
 QY 481 CTCAGCTGCGCTTACAG 540  
 Db 11658 CTCAGCTGCGCTTACAG 11599  
 QY 541 CCTCTGCTGCTGAGGAG 600  
 Db 11598 CCTCTGCTGCTGAGGAG 11539  
 QY 601 TTCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Db 11538 TTCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11479  
 QY 661 GGGGAGAGACATCTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 Db 11478 GGGGAGAGACATCTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11419  
 QY 721 CACAGAGATTTTCCCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 Db 11418 CACAGAGATTTTCCCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11359  
 QY 781 TGACTCAGCTCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 Db 11358 TGACTCAGCTCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11299  
 QY 841 CCCCCCTGAGAGACTAGAGACTTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
 Db 11298 CCCCCCTGAGAGACTAGAGACTTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11239  
 QY 901 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 Db 11238 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11179  
 QY 961 ATGCTCAGTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 Db 11178 ATGCTCAGTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11119  
 QY 1021 TGACTCTTCTTTCAGAGCGCCCGCCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 Db 11118 TGACTCTTCTTTCAGAGCGCCCGCCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 11059  
 QY 1081 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Db 11058 GAGGCGACCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10999  
 QY 1141 CAGCGGAGTGGGAG 1200  
 Db 10998 CAGCGGAGTGGGAG 10939  
 QY 1201 GATGAGACCTTCCAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAC 1260  
 Db 10938 GATGAGACCTTCCAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAC 10879  
 QY 1261 ACCTGCGATGCTGAG 1320  
 Db 10878 ACCTGCGATGCTGAG 10819  
 QY 1321 GAGAGATGAGAGATGATGCTGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
 Db 10818 GAGAGATGAGAGATGATGCTGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10759  
 QY 1381 GGTGCTGCTGAGGCTGAG 1440  
 Db 10758 GGTGCTGCTGAGGCTGAG 10699  
 QY 1441 CTTCCTTGCACATCCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1500



XX Sequence 4003 BP: 797 A; 1116 C; 1204 G; 886 T; 0 other;

Query Match 74.9%; Score 1829; DB 24; Length 4003;  
 Best Local Similarity 88.3%; Pred. No. 0;  
 Matches 2181; Conservative 0; Mismatches 245; Indels 45; Gaps 16;

3 CTCCGAGTCTCGGATCTGGATGATCCACCCGAGGCGCGGACCCGACGACTCTTA 62  
 1061 CCCGATGATCTCCGGATCCAGATCGACCCGAGGCTGGGGACCTGCAAGATGCTTCA 1120  
 63 CCTGGGAACACCCCAAGGCGCTTTA-----CCAAATATCCCG 100  
 1121 CCCGGAGAGGCCAGGCGCTTTACCTGTTTATCTTCACTTGAAGGCTCAAAATATTCG 1180  
 101 CGGATGGTCCGGGAGGAGGCGGCTGGTGGGCGGGCTGACGAGGAGGAGTGGGCGCA 160  
 1181 CAGGTGCTAGGGGCGGGCGGCGGCTGGTGGGCGGGCTGACCGGGGAACTGGGCGCA 1240  
 161 GGTTCACACCTTCAGTGTGATTTGGCTGGGCTGGGCTCCGACGAGGAGGCTCTTC 220  
 1241 GGTTCACACCTTCAGTGTGATTTGGCTGGGCTGGGCTCCGACGAGGAGGCTCTTC 1300  
 221 CGCGGATGAAAGATGATGCTTACGATGCAAGGATTAACCTGCGCTGAAAGAGGACTG 280  
 1301 CGCGGATGAAAGATGATGCTTACGATGCAAGGATTAACCTGCGCTGAAAGAGGACTG 1360  
 281 CGCTCTCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 340  
 1361 CGCTCTCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1420  
 341 AATGAGTGAACAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 400  
 1421 AATGAGTGAACAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1480  
 401 TACCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 460  
 1481 CACCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1540  
 461 CCCTGATCTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 520  
 1541 GGTGATCTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1600  
 521 CACGACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 580  
 1601 CACGACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1660  
 581 GATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 638  
 1661 GATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1720  
 639 ATGAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 698  
 1721 ATGAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1780  
 699 TTGAGCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 757  
 1781 TTGAGCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1840  
 758 CACGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 817  
 1841 CACGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 877  
 818 GGTCAAGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 837  
 1899 GATTAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 897  
 878 GATTAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 937  
 1959 GATTAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 997  
 938 CAGTATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 997

2019 CAGGTGCTATTCAC---TCAGGATGTCACAT--GGGGCTGCTGGGCTGCCATGAG 2073  
 998 AGATGCAAAAGTGTGATTTTCTGACTCTCTCTTTCAGA--CCCCCAAGACACAGTGT 1056  
 2074 GAATGCAAAAGTGTGATTTTCTGACTCTCTCTTTCAGA--CCCCCAAGACACAGTGT 2133  
 1057 ACCGACCAAGGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1116  
 2134 ACCGACCAAGGCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2190  
 1117 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1176  
 2191 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2250  
 1177 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1236  
 2251 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2310  
 1237 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1296  
 2311 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2370  
 1297 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1355  
 2371 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2430  
 1356 GAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1415  
 2431 GAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1475  
 1416 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1535  
 2490 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1595  
 1476 GCTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1655  
 2550 GCTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1715  
 1536 GAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1775  
 2610 GAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1835  
 1596 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1895  
 2670 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1955  
 1656 CACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2015  
 2730 CACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2075  
 1716 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2135  
 2789 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2195  
 1776 AGTATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2255  
 2849 AGTATATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2315  
 1836 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2375  
 2908 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2435  
 1894 ATTTCTGAAAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2495  
 2968 ATTTCTGAAAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2555  
 1954 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2615  
 3028 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2675  
 2014 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2735  
 3088 CTTGCGAGATTCATCTGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2795

OY 2074 TTGGGAG-CCATGGGGGAGCTACCCACCACCAATTCCTCTGTGGCCACATCTCTGT 2132  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3148 TTGGGAGCCCAATGGGGAGCTACCCACCACCAATTCCTCTGTAGCCACATCTCTGT 3207  
OY 2133 GGTCTTGACCAAGTGTCTTTTCTTACTCTAGGAGTACAGTCCACAGGCTCTA 2192  
|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3208 GGGATCTGACAGTCTGTCTTTTCTTACCCAGGAGCCAAAGTCCACAGGCTCTG 3267  
OY 2193 ATGTCTCTCAGGCTGTAAATGTGACACCCGGGGGCTGTATGTGTGTGTGT 2252  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3268 ATGTCTCTCAGGCTGTAAATGTGACACCCCTGGAGGCTGTATGTGTGTGTGT 3327  
OY 2253 GAGGGACACGAGGACATAGTGTCTATAGAGTCTTTCACCTTCATATATAGCAT 2312  
| ||| ||||| ||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3328 G-GGGTAACAGTGAATATAGTGTGTATGGGTTCTTGACTTGATATCAGCAC 3386  
OY 2313 GTGATGGGCTGTTTAAAGTGTACCCCTGACTGTGATGTGAATTTGTTCATGTA 2372  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3387 ATGATGGGCTGTTCAGAGGTGTACCCCTCAGTGTAGATATGAAATTTGTTCATGATA 3446  
OY 2373 -TTTTCTGTAGTGAACAGCTGCCCTGTGTGGACTGATGGCAAGATTTGTTCATG 2431  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
DB 3447 TTTTCTTATAGTGTAGACAGCTGCTTGTGTGGACTGAGAGCAAGATTTGTTCATG 3506  
OY 2432 CCTTCCCTTTG 2442  
||||| |||||||  
DB 3507 CCTTCCCTTTG 3517

RESULT 7  
ID ABA18125 standard; DNA; 3098 BP.

XX ABA18125;

DT 23-JAN-2002 (first entry)

XX Human nervous system related polynucleotide SEQ ID NO 10456.

XX Human: nootropic; neuroprotective; cytosolic; dermatological; virocidic;  
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;  
XX antiParkinsonian; antisickling; antianemic; antiarthritic; cancer;  
XX antilethemic; hepatotropic; cerebroprotective; antiinflammatory;  
XX antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;  
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX Homo sapiens.

XX WO200159063-A2.

XX 16-AUG-2001.

PE 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225287.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 16-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 06-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231245.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231966.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 20-OCT-2000; 2000US-0242221.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249219.  
 PR 17-NOV-2000; 2000US-0249224.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 01-DEC-2000; 2000US-0251160.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0251989.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI: 2001-541565/60.  
 XX  
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating nervous system  
 PT cancers and metastases -  
 XX  
 PS Disclosure: SEQ ID NO 10456; 1701tp + Sequence Listing: English.  
 XX  
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins  
 CC (ABA14678-ABA18001) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://ftp.wipo.int/pub/published_pat_sequences).

XX Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other;

Query Match 63.6%; Score 1554; DB 22; Length 3098;  
 Best Local Similarity 82.5%; Pred. No. 0;  
 Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20.

QY 1 TACTCCGAGTCTCCGGCTGTGGATCCACCCGAGGCGGAGCCGCCAAGACCTTC 60  
 Db 551 TCCCTCAGAGTCTCCGGATCTACCCGAGGAGGAGCCGCCAAGACCTTC 620  
 QY 61 TACCTGGAGAGACCCCAAGGGGCTTTA-----CCAAATGCC 98  
 Db 621 CACCCGAGAGTCCCGAGGCGCTTACCCAGGTTATTTCAGTTAGGCCAATTC 680  
 QY 99 CGGGGTGGTCCGGGCGAGGCGAGGCTGGTGGCGGGCTGACCGAGGAGGCGG 158  
 Db 681 CGGGGTGGGCGGGGAGGCGGGGCTAGTGGCGGGGCTGACTG-CGGGAGACGGC 739  
 QY 159 CAGTTCTCACACCTTCAGTGATGATGTCGCGGACCTGGGGTCCGAGACGCTTC 218  
 Db 740 TAGGCTCTACACCTTCAGGATGATGCTGCGAGTGGGCGCGGAGGAGGCTTC 799  
 QY 219 TCCGGGGTATGAACATGATGCTGATGATGCAAGATTAATCTGCTGAAAGAGACC 278  
 Db 800 TCCGGGGTATGACATGATGATGATGATGATGATGATGATGATGATGATGATG 859  
 QY 279 TGGCTCTCGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338  
 Db 860 TGGCTCTCGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 919  
 QY 339 CCAATGTGGCTGAACAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
 Db 920 AGGAATATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 979  
 QY 399 GATACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 458  
 Db 980 GATACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1038  
 QY 459 CTCCTGATCTCTGAGAGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 518  
 Db 1039 CTCCTGATCTCTGAGAGCTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1098  
 QY 519 ACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578  
 Db 1099 CCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158  
 QY 579 CAGATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 638  
 Db 1159 GAGATCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1218  
 QY 639 ATGAAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 698  
 Db 1219 ATGAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1277  
 QY 699 TTTGA-CCCCACACACCTTTGGACAGGAGCTTTTCCCTCAGGCTTCTGTGCT 757  
 Db 1278 TTTGAGCCCTCCACACAGCTTTGGGCCCCGTTGACTTTTCTGCAAGTTCTGTGCT 1337  
 QY 758 CACACTCAATGTGTGGGGGTCTGACTCCAGTCTCTGAGTCCCTTGGCTCCACTCA 817  
 Db 1338 CACACTCAATGTGTGGGGGTCTGACTCCAGTCTCTGAGTCCCTTGGCTCCACTCA 1387  
 QY 818 GGTAGACACCGAGGAGTCTGCTCCCGCTCAGAGACTGAGACTTTCCAAAGAAATAGA 877  
 Db 1388 GGTAGAGGCGAGAGTCTGCTCCCGCTCAGAGACTGAGACTTTCCAAAGAAATAGA 1446  
 QY 878 GATATCTCCAGGCTCCGCTGCTCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 937  
 Db 1446 GATATCTCCAGGCTCCGCTGCTCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT

```

Db 1447 GATTTCACAGTGTCTGTGTCACAGGCTGTGTGTTCTGTGCTCTCCCTCCCAACC 1506
OY 938 CAGGTATCTGTTCTTATGATGTGTACATCCAGATGCTGGATGCTCCCATAG 997
    ||||| || || ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1507 CAGGTGCTGCTGATCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1554
OY 998 AGATGCAAGTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1057
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1565 GAGTCAAGTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1621
OY 1058 CCGACCAAGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1622 CCGACCAAGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1681
OY 1118 CCGACCAAGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1682 CCGACCAAGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1741
OY 1178 TCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1742 TCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801
OY 1238 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1802 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1861
OY 1298 TCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1862 TCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1921
OY 1340 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1922 TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1981
OY 1400 GGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1982 AGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2041
OY 1460 CATCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2042 CATCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2101
OY 1520 CGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2102 CGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
OY 1580 AGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2161 AGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2220
OY 1640 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2221 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
OY 1700 CTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1759
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2281 CTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
OY 1760 ATG--GGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1816
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2341 GTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
OY 1817 CTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2401 CTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
OY 1875 CTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1934
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2461 CTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
OY 1935 TCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1994
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2521 TCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580

```

```

OY 1995 ATTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2054
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2581 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2639
OY 2055 GATTCCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2640 GATTCCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2699
OY 2114 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2173
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2700 -----TAGCCATATCTGTGGCTGTGACAGAGCTGTGTTTGTCTTCTACCAATCACT 2753
OY 2174 GACAGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2754 GACAGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2813
OY 2229 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2814 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2873
OY 2286 TTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2874 TTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2933
OY 2346 TGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2404
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2934 TGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2993
OY 2405 GGGAGTGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2424
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2994 GGGAGTGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3013

RESULT 8
AAS40421
ID AAS40421 standard; DNA; 3098 BP.
XX
AC AAS40421;
XX
DT 17-DEC-2001 (first entry)
XX
DE DNA encoding human prostate cancer antigen, Seq ID No 573.
XX
KW Human; prostate cancer antigen; cytosolic; uropathic; diagnostic;
KW reproductive system; chromosomal marker; forensic; urinary disorder;
KW chronic nephritis; blood-related disorder; thrombosis; ds.
XX
OS Homo sapiens.
XX
PN WO20015316-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01328.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.

```



PR 26-JUL-2000; 2000US-0220964.  
 PR 14-AUG-2000; 2000US-0224518.  
 PR 14-AUG-2000; 2000US-0224519.  
 PR 14-AUG-2000; 2000US-0225213.  
 PR 14-AUG-2000; 2000US-0225214.  
 PR 14-AUG-2000; 2000US-0225266.  
 PR 14-AUG-2000; 2000US-0225267.  
 PR 14-AUG-2000; 2000US-0225268.  
 PR 14-AUG-2000; 2000US-0225270.  
 PR 14-AUG-2000; 2000US-0225447.  
 PR 14-AUG-2000; 2000US-0225757.  
 PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226688.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235184.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239335.  
 PR 13-OCT-2000; 2000US-0239337.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246529.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246533.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0251989.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX  
 PT Rosen CA, Barash SC, Ruben SM;  
 PI WPI; 2001-451929/48.  
 DR  
 XX  
 XX  
 PT Isolated polypeptide for treating, preventing and/or prognosing  
 PT disorders related to the reproductive system including prostate cancer  
 PT and also for testing and detection e.g. diagnosis -  
 XX  
 PS Disclosure; SEQ ID No 573; 546pp; English.  
 XX  
 CC The invention relates to novel isolated human prostate cancer antigen  
 CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for  
 CC preventing, treating or ameliorating a medical condition when  
 CC administered. (I), (II) and the antibody to (II) are useful for treating,  
 CC preventing and/or prognosing disorders related to the reproductive  
 CC system including prostate cancers; urinary disorders e.g. chronic  
 CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used  
 CC for testing and detection e.g. as a chromosomal marker and in forensics.  
 CC (I) and the anti-(II) antibody can be used in testing and detection in  
 CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer  
 CC antigen coding sequences, and related PCR primers and sequences of the  
 CC invention. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at: ftp.wipo.int/pub/published\_pct\_sequences.





OY 2055 GATCCTTGAGATCTGTGTTGGAGCC-ATGGGGAGCTCACCCACCCACATTCCTC 2113  
DB 2640 GATTGTTGGATATTGGTATGAGAGGAGCTATGAGGAGGAGCTCACCCACCCACATTCCTC 2699  
OY 2114 CTGTCGACATCTCTCTGTGCTGTGACCAAGTGTCTGTTTGTCTACTTACGCACT 2173  
DB 2700 -----TAGCCACATCTGTGCTGTGACCAAGTGTCTGTTTGTCTACTTACCCACATTCCT 2753  
OY 2174 GACAGTGGCCAGGCTCTAATGTGCTCTCAGGCTGTAAAGTGTACACCC-----CGG 2228  
DB 2754 GACAGTGGCCAGGCTCTGAGGCTGTCTCTCTCAGCTATATAGGTGACCTCTCAGGCA 2813  
OY 2229 GGGGCTGATGTGTGTGGGTTGTGAGGGG---AACAGGGACATACCTGCTATGAG 2285  
DB 2814 GGGGCTGATGTGTGTGGGTTGTGAGGGGAAACAGAGGAGCTCAGCTGCTATGAG 2873  
OY 2286 TTCTCTGATCTCAATGATGATGACATGATGAGGCTGTAAAGTGTCTCAGCTGAG 2345  
DB 2874 TTCTCTGATCTGATGATGATGACATGATGAGGCTGTAAAGTGTCTCAGCTGAG 2933  
OY 2346 TGACTGATATGATTTTGTTCATGATATTTT-TCTGTAGTGTGAACAGCTGCCCTGTG 2404  
DB 2934 TGACTGATATGATTTTGTTCATGATATTTTCTCTATAGTGTGACAGCTTCTTGTG 2993  
OY 2405 GGGAGTGTGCAAGATT 2424  
DB 2994 GGGAGTGTGCAAGATT 3013

RESULT 9  
ID AAL04024 standard; DNA: 3098 BP.  
AC AAL04024:  
XX 21-NOV-2001 (first entry)  
XX Human reproductive system related antigen DNA seq ID NO: 6712.  
DE Human reproductive system related antigen; reproductive system disorder;  
XX cancer; gene therapy; ds.  
OS Homo sapiens.  
XX  
XX  
XX WO20015320-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01339.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217486.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 21-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234224.  
PR 25-SEP-2000; 2000US-0234977.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 29-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239835.  
PR 13-OCT-2000; 2000US-0239837.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.



```

Db 1742 TTGTGGACACCGGCTGCGAGGGATGGAACTTCCAGAAAGTGGCCGCTGTGGTGGTGC 1801
Oy 1238 CTTTCAGAGAGAGACAGATATACAGTGCATGTGACAGCATGAGGGGCTGCCGAGCCCC 1297
Db 1802 CTCCGTGAGAGAGACAGATATACAGTGCATGTGACAGCATGAGGGGCTGCCGAGCCCC 1861
Oy 1298 TCATGCTGAGATGAGATGAGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGATGAG 1339
Db 1862 TCATGCTGAGATGAGATGAGAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGATGAG 1921
Oy 1340 CTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
Db 1922 TTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1981
Oy 1400 GGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
Db 1982 AGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2041
Oy 1460 CATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
Db 2042 CATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2101
Oy 1520 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
Db 2102 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Oy 1580 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1639
Db 2161 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Oy 1640 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1699
Db 2221 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Oy 1700 CTCTTTTGAAGACCTGTGACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1759
Db 2281 CTCAATTTTGAAGACCTGTGACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Oy 1760 ATG - GGGACCTGATCCAGTATGACAGAGTCA - GGAAGAGTCCCTGCTGAGAGAG 1816
Db 2341 GTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Oy 1817 CCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1874
Db 2401 CCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Oy 1875 CCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1934
Db 2461 CCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 2520
Oy 1935 TCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1994
Db 2521 TCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Oy 1995 ATTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2054
Db 2581 ATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2639
Oy 2055 GATTCCTGGAGATCTTGTGTTGGAGCC - ATGGGGAGCTCCACCCACACCAATTCCTC 2113
Db 2640 GATTCCTGGAGATCTTGTGTTGGAGCC - ATGGGGAGCTCCACCCACACCAATTCCTC 2699
Oy 2114 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2173
Db 2700 -----TACCACATCTGTGGGCTGACAGGTCCTGTTTGTGTCTACCCCAATCAGCT 2753
Oy 2174 GACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2228
Db 2754 GACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2813
Oy 2229 GGGGCTGATGCTGTGGGTTGGAGGG - AACAGGGAGACATAGCTGCTATGAGAG 2285

```

```

Db 2814 GGGCCCTGATGTGAGTGGGGGTGTGGGGGGAACAGAGGGGACTCAGCTGTGCTATTGGC 2873
Oy 2286 TTTCCTTTGACTTCATATGTTTGTGACATGTGATGGGCTTTTAAAGTGTACACCCCTACTG 2345
Db 2874 TTTCCTTTGACTTCATATGTTTGTGACATGTGATGGGCTTTTAAAGTGTACACCCCTACTG 2933
Oy 2346 TGACTATATGATTTGTTGATGATATATTTT - TCTGTAGTGTGAAGACGTGCTGTGT 2404
Db 2934 TGACTATATGATTTGTTGATGATATATTTTCTGTATAGTGTGAGACAGCTCTCTGTGT 2993
Oy 2405 GGGACTGAGTGGCAGATTT 2424
Db 2994 GGGACTGAGTGGCAGATAT 3013

RESULT 10
AAK86871
ID AAK86871 standard; DNA; 3038 BP.
AC AAK86871;
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41683.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225457.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0226279.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.

```

PR	1-SEP-2000	2000US-0229343
PR	01-SEP-2000	2000US-0229344
PR	01-SEP-2000	2000US-0229345
PR	05-SEP-2000	2000US-0229509
PR	05-SEP-2000	2000US-0229513
PR	06-SEP-2000	2000US-0230437
PR	06-SEP-2000	2000US-0230438
PR	08-SEP-2000	2000US-0231242
PR	08-SEP-2000	2000US-0231243
PR	08-SEP-2000	2000US-0231244
PR	08-SEP-2000	2000US-0231413
PR	08-SEP-2000	2000US-0231414
PR	08-SEP-2000	2000US-0232080
PR	08-SEP-2000	2000US-0232081
PR	12-SEP-2000	2000US-0231968
PR	14-SEP-2000	2000US-0232357
PR	14-SEP-2000	2000US-0232358
PR	14-SEP-2000	2000US-0232399
PR	14-SEP-2000	2000US-0232400
PR	14-SEP-2000	2000US-0232401
PR	14-SEP-2000	2000US-0233063
PR	14-SEP-2000	2000US-0233064
PR	14-SEP-2000	2000US-0233065
PR	21-SEP-2000	2000US-0234223
PR	21-SEP-2000	2000US-0234225
PR	21-SEP-2000	2000US-0234274
PR	25-SEP-2000	2000US-0234997
PR	25-SEP-2000	2000US-0234998
PR	26-SEP-2000	2000US-0235484
PR	27-SEP-2000	2000US-0235834
PR	27-SEP-2000	2000US-0235836
PR	29-SEP-2000	2000US-0236327
PR	29-SEP-2000	2000US-0236367
PR	29-SEP-2000	2000US-0236368
PR	29-SEP-2000	2000US-0236369
PR	29-SEP-2000	2000US-0236370
PR	29-SEP-2000	2000US-0236802
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	02-OCT-2000	2000US-0237043
PR	13-OCT-2000	2000US-0239937
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241221
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241809
PR	20-OCT-2000	2000US-0241826
PR	01-NOV-2000	2000US-0244671
PR	01-NOV-2000	2000US-0244674
PR	08-NOV-2000	2000US-0246475
PR	08-NOV-2000	2000US-0246476
PR	08-NOV-2000	2000US-0246477
PR	08-NOV-2000	2000US-0246478
PR	08-NOV-2000	2000US-0246523
PR	08-NOV-2000	2000US-0246524
PR	08-NOV-2000	2000US-0246525
PR	08-NOV-2000	2000US-0246526
PR	08-NOV-2000	2000US-0246527
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610
PR	08-NOV-2000	2000US-0246611
PR	08-NOV-2000	2000US-0246613
PR	17-NOV-2000	2000US-0249207
PR	17-NOV-2000	2000US-0249208
PR	17-NOV-2000	2000US-0249209
PR	17-NOV-2000	2000US-0249210
PR	17-NOV-2000	2000US-0249211
PR	17-NOV-2000	2000US-0249212

Query Match	Best Local Similarity	Matches 2047;	Conservative	Score 1554;	Pred. No. 0;	DB 22;	Length 3098;	Mismatches 350;	Indels 83;	Gaps 20
QY	1	TACATCCGAGTCCTCGGCTGTGGATCCACCCGAGGCGCGGAGCCCGCCAGACCTTC	60							
DB	561	TCCTCTAGAGTCTTCGGATCCGAATATACCCGAGGCGAGCGGAGCCCGCCAGACCTTC	620							
QY	61	TACCTGGAGACCCCAAGCGGCTTTA-----CCAATATCC	98							
DB	621	CACCGGAGAGTCCGAGCGGCTTTACCCAGGTTCTATTTCAGTTAGGTCCAAAATCC	680							
QY	99	CGCGGAGTGGTCCGGGCGAGGCGAGGCTCGTGGGCGGGGCGAGCGAGGGGTTGGGG	158							







Db	2153	CACACTCAATGTGTGTTGGGCTCTGAAATTCC-----AGTCCCTGGGCTCCACTTA	2202
QY	818	GGTCAGAAACCGGAGGTCCCTGCTCCCCCTCAGAACCTTAAGAACTTTCCAGGAATAGGA	877
Db	2203	GGTCAGAGGCCAGAAAGTCCCTGCT-----CCCACTCAGAACCTTCCAGGAATAGGA	2261
QY	878	GATTATCCCAAGTCCCGCTGTCCAGAGCTGGTGTCTGGTTCGTGCTGCCCTTCCACACC	937
Db	2262	GATTTTCCAGAGTGTCTGTGTCCAGAGCTGGTGTCTGGTTCGTGCTGCCCTTCCACACC	2322
QY	938	CAGGTATCTGGTTCATTCCTTAGATGTGTACATCCAGGTCTCTGTGAGTGTCCATAG	997
Db	2322	CAGGTCTCTCTCCATTCCTTAGGTGTGTACAT--GGGTCTGTGGGGTTCCTCATAG	2379
QY	998	AGATGCAAAGTCTTGAATTTTCTGACTCTTCTTCAACACCCCCCAAGACACACGTGA	1057
Db	2380	GAGTGCAAAGTCCCTGAATTTTCTGACTCTCT--TCAGATCTCCAAAGGACACAGTGG	2438
QY	1058	CCCAACACCCGTCTTTGACTATGAGGCCACCTGAGGTCTGTGGGCCCTTGGCTTCTAC	1117
Db	2437	CCCAACACCCCATCTCTGACCTATGAGGCCACCTGAGGTCTGTGGGCCCTTGGCTTCTAC	2488
QY	1118	CTGGGAGATCATCTACCTGTGCAGCGGAGTGGGAGAGACAGACCAGACCTGTAGAC	1177
Db	2497	CTGGGAGATCATCCTGACCTGGAGCGGAGTGGGAGAGACAGACCAGACACAGAC	2556
QY	1178	TCGTGTGAGACCAAGCCCTGTGAGGGGATGTGAACTTCCAGAAATGTGGACGTGTGTGTGC	1237
Db	2557	TTGTGTGAAACCAAGCCCTGTGAGGGAGTGTGAACCTTCCAGAAATGTGGGCCGTGTGTGTGTGC	2618
QY	1238	CTTGTGAGAGAGACACAGATATACAGTGCATGTGACATGAGGGGTGCGCGGAGGCC	1297
Db	2617	CTTGTGAGAGAGACACAGATATACAGATGCATGTGACAGAGGGGTGCGCGGAGGCC	2678
QY	1298	TCATGCTCAGATGTGAGTAAAGAGGGAGAT-----GGAGGCATCATGT	1339
Db	2677	TCATGCTCAGATGTGAGTAAAGAGGGAGATGGTAAAGGGGACAGAGGGGTCACTGTCTT	2736
QY	1340	CTGTAGGAGAAAGCAGGAGCCCTCTGTGAACACCTTTAACAGGATCGGTGTGAGGGCTGG	1399
Db	2737	TTTCAGAGGAAAGCAGGAGCCCTTCTGTGACCTTTCAGAGGGTCAAGGCTGAGGCTGG	2796
QY	1400	GGGTGAGAGACCCCTCACCTTACCTCTTCCCAAGACAGTCCCTGCCACCATATCC	1455
Db	2797	AGATCAGGGGCCCTCACCTTCCCTTCTTCCCAAGACATCTCCCCAGGCCACATATCC	2856
QY	1460	CATCATGGGATTCGTGCTGTGAGCTGTGTCTTCTTGCAGCTGATCATGTGAGCTGGAT	1519
Db	2857	CATCTGTGGCATTCGTGCTGTGAGCTGTGTCTTCTTGTGAGCTGTGTGCTACTGTGAGCTGTGGT	2918
QY	1520	CGCTGCTGTGTGTGAGAAAGAACCTCATGTTAAGAAAGGGGTGTACAAAGTGGGTGTG	1579
Db	2917	CGCTGCTGTGTGTGAGAAAGAACCTCATGT--AGCAAGGGGTGTAGAGATGTGAGTGTG	2975
QY	1580	AGTTTTCTTGTCCACTGGGGGTTTCAAGCCCCAGGTAAAGTGTGCTGCTGCTGTTTAC	1639
Db	2976	AGTTTTCTTGTCCACTGGGGGTTTGTGCAAGCCCAAGTAAAGTGTGCTGCTGCTTATTAC	3038
QY	1640	TGGGAAGCACCATCCACATCATGTGGGCTTACCCAGGCTGGGCCCTGTGTCAGACCTT	1699
Db	3036	TGGGAAGCACCATCCACATCATGTGGTCTTCCAGGCTGGGCCCTGTGTGTGCCAGCACTA	3099
QY	1700	CTCTTTTGTAAAGCACTGTGACATGACAGCAGATTTATTTACTTGTATGTATGTAGT	1758
Db	3096	CTCATTTTAAAGCTCTCTGTGAATTTGAAGACAGATCTTCACTCTGATGTATGTAGT	3155
QY	1760	ATG--GGGACCTGTATCCAGTAATCAAGGTCA--GGAGAAGGTCCTGTGCTTAAGACAGA	1818
Db	3156	GTGATGGGACCTGTATCCAGAGTCAACAAATCAAGGGAAGGTCCCTGTCTATATACAGA	3215
QY	1817	CCTTAAGAGGCACTGTGTGAGGACCAATCTGCTTTCCTTGTTTTCCGTGATC--GC	1874

Db	3216	CCCTGAGAGGGGACGTTGGTCCACGAGACCCACATCTGCTTTCCTTCATATTCTCATACCTGCG	3275
QY	1875	CCCTGGGCTCTGCATGCACACATTTCTTG6AAACTCTTCGAGGGTCCAAACATGAGAGTTC	1934
Db	3276	CCCTGATCTACAGTTCACACTTTCCTTG6AAACTCTCTGGATCAAAAGCATGGGGTTGC	3335
QY	1935	TCTTGGACCTCATAGGCCCTCCGCCACCTTTCCTGCTCTCCACAGCAATTTTCTCCACAG	1994
Db	3336	TCTGATGACCTTATAGCCCTCCGCCCTTCTTCTGCTCTCCACAGCAATTTTCTCCACAG	3395
QY	1995	ATTGAAAAGGAGGAGGAGCTATCTCAGGCTGCAAGTAAGTATGAGGAGGCTGATCCTCTGA	2054
Db	3396	ATTGAAAACAGAGGAGGAGCTATCTCAGGCTGCAAGTAAGTATGAGGAGGCTGATCCTCTGA	3454
QY	2055	GATCCTTGGGATCTTGTGTGTTTG6AGCC-ATG6GGAGCTCACCCACCCACAATTCCTC	2113
Db	3455	GATTCGTTGGGATCTTGTGTGTTTG6AGCCATATGAGGAGCTCACCCACCCACAATTCCTC	3514
QY	2114	CTCTGGGCACATCTCCTCGTGTCTCTGACACAGTCTGTTTTTGTCTACTCTAAGGAGT	2173
Db	3515	-----TAGCCACATCTGTGGGCTCTGACACAGTCTGTTTTTGTCTACTCTAAGGAGT	3568
QY	2174	GACAGTCCCCAGGAGCTCTATGTGTCTCTCAGCGCTTGTAAATGTGACACC-----CGG	2228
Db	3569	GACAGTCCCCAGGAGCTCTGTGGGCTCTGACACAGTCTGTTTTTGTCTACTCTAAGGAGT	3628
QY	2229	GGGGCCGATGTGTGTGTGGTGTGTGAGGGG---AACAAGGAGCAATCTGTGCTATGAGG	2285
Db	3629	GGGGCCGATGTGTGTGTGGTGTGTGAGGGGAGACAGAGGGAGCTGAGTGGCTATGGG	3688
QY	2286	TTTCTTTGACCTCAATGTATTTAGCATGTGATGGGCTGTTTAAAGTGTCAACCCCTCACTG	2345
Db	3689	TTTCTTTGACCTGAGTATGTCTTGAGCATGAAATGGGCTTTTAAAGTGTCAACCCCTCACTG	3748
QY	2346	TGACGTGATGAAATTTGTTCATGAATATTTT--TCTGTAGTGGAAACAGCTGGCCCTGTGT	2404
Db	3749	TGACGTGATGAAATTTGTTCATGAATATTTTCTCTATATGTGTGAGACAGCTTCTTGTGT	3808
QY	2405	GGGAGCTGAGTGCCAGATTT 2424	
Db	3809	GGGAGCTGAGAGCAAGATAT 3828	
RESULT 12			
ABN97218			
ID	ABN97218	standard; DNA; 4316 BP.	
XX	AC	ABN97218;	
XX	DT	13-Aug-2002 (first entry)	
XX	DE	Gene #3716 used to diagnose Liver cancer.	
XX	KM	Gene; Liver cancer; ds; hepatocellular carcinoma; hepatotropic;	
XX	KW	metastatic liver tumor; cytostatic; expression profile; disease state;	
XX	KX	disease progression; drug toxicity; drug efficacy; drug metabolism.	
OS		Homo sapiens.	
XX	PN	WO200229103-A2.	
PD	XX	11-Apr-2002.	
XX	PF	02-Oct-2001; 200LMO-US30589.	
XX	PR	02-Oct-2000; 200OUS-237054P.	
XX	PA	(GENE-) GENE LOGIC INC.	
PI	XX	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;	
XX	DR	WPI: 2002-426119/45.	
XX			

PT Diagnosing and detecting the progression of liver cancer,  
PT hepatocellular carcinoma or metastatic liver tumor in a patient,  
PT involves detecting the level of expression of two or more genes in a  
PT liver tissue sample

XX Claim 1: SEQ ID NO 3716; 298bp; English.

XX The invention relates to a novel method for diagnosing and detecting the  
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver  
CC tumour in a patient, and differentiating metastatic liver cancer from  
CC hepatocellular carcinoma in a patient, involving detecting the level of  
CC expression of two or more genes represented in ABN93503-ABN97455 in a  
CC tissue sample. The method of the invention has hepatotropic, and  
CC cytosolic activity. The method is useful for diagnosing and detecting  
CC the progression of liver cancer, hepatocellular carcinoma and metastatic  
CC liver carcinoma in a patient. The method is useful for identifying  
CC expression profiles which serve as useful diagnostic markers as well as  
CC markers that can be used to monitor disease states, disease progression,  
CC drug toxicity, drug efficacy and drug metabolism.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.

XX Sequence 4316 Bp: 1000 A: 1090 C: 1292 G: 934 T: 0 other:

Query Match 63.5%; Score 1551.6; DB 24; Length 4316;

Best Local Similarity 82.7%; Pred. No. 0; Mismatches 344; Indels 84; Gaps 21;

Matches 2052; Conservative 0; Mismatches 344; Indels 84; Gaps 21;

QY 1 TACTCCGAGTCTCCGGGTCTGGATCCACCCGAGGCGCGGAGACCCGACGACCTTC 60  
DB 1377 TCCCCCGAGTCTCCGGATCCGAATCTACCCCGAGGCGAGC-GGACCGCGCAGACCTTC 1435  
QY 61 TACCTGGGAGAACCCCAAGGCGCTTTA-----CCAAATCCC 98  
DB 1436 CACCCGAGAGTCCGAGCGCGCTTACCGAGGTTCAATTTAGGCGCAAAATCCC 1495  
QY 99 CCGGGGTGGGTCCGGCGAGGGGCGAGGCTCGGTTGGGCGGCGGCGAGCCGAGGAGGAGC 158  
DB 1496 CCGGGTTGGCGGGGAGGGGAGGCTAGCTGGGCGGCGCTGACTG-CGGGAGACGGC 1554  
QY 159 CAGGTTCTACACCTCTCAGTGTGATTTGGCTGCAGCTGGGGTCCGAGCGACGCTTC 218  
DB 1555 TAGGTTCTACACCTCTCAGGGAATGATGGCTGCAGCATGGGCGCGAGCGCGCTTC 1614  
QY 219 TCCGCGGGATGACAGTATGCTTACGATGGCAGGATTAATCTCGCCCTGAACGAGGACC 278  
DB 1615 TCCGCGGGATGACAGCGAGCTTACGAGCGCAAGGATTAATCTCTGTAACGAGGACC 1674  
QY 279 TGGGCTCTGGAGCGGAGGACACTCGGCTCAGATCTCCAAAGCCAGTGTGAGGCGG 338  
DB 1675 TGGGCTCTGGAGCGGCGGAGACCGTGGCTCAGATCCAGCGCTTCTAGAGGCGAG 1734  
QY 339 CCAATGTGGCTGAACAAAGAGAGCCTACCTGAGGGCGACGTCGTGAGTGGCTCCACA 398  
DB 1735 AGGAATGTGAGAGGAGTTCAGGAGCTACCTGAGGGCGAGTCTGAGTGGCTCCGGA 1794  
QY 399 GATACCTGGAGAACGGGAAGAGATGTGAGGCGCGGGTACCAAGGGGAGAGGGGCGG 458  
DB 1795 GATACCTGGAGAACGGGAAGAGACGTACAGCGGAGGTACCAAGGGGCGCAT-GGGCGC 1853  
QY 459 CTCCTGTATCTCTGTAGACCTCTCAAGCCTGGCTAGCACAAAGAGAGAGAAAAATGGG 518  
DB 1854 CTTCCTATCTCTCTGTATGATCTCTGGGATGGCTGCGACAAAGGTTGGGAGAAATGGG 1913  
QY 519 ACCAACAAGTAAATATGCGCTCCCTCTGTCTGAGGAGAGAGATCTCTGGGTTTC 578  
DB 1914 CCAATCTAGATATATGCGCTCCCTCTGTAGTGAAGAGAACTTCTGGGCTTTC 1973  
QY 579 CAGATCTGTACAGAGAGATGATTTGAGGCGCGCTCTCTCTGAGCAATTAAGG 638  
DB 1974 GAGATCGGTACAGAGAGTACTGTAGAGTCCGCCCTGCTCTGTGGACAAATTAAGG 2033

QY 639 ATGAGTCTCTGAGGAGTGGAGGAGAACAAATCCCTGGAAAGTATGATAGGGTTCCC 698  
DB 2034 ATGAATCTCTGAGGGAATGGA-GGGAAGACATCTCCCTGGAAATACGATCCGGGTTCCC 2092  
QY 699 TTTGA-CCCCACAGACAGCTTGGCACCAGGACATTTTCCCTCAGGCTTGTCTGCTCT 757  
DB 2093 TTTGAGCCCTCCAAACAGCCTTGGGCCCCGAGCTTTTCTCAAGTTTGTCTGCTCT 2152  
QY 758 CACACTAATGTGTGTGGGGGTCTGACTCCAGCTCTCTGAGTCCCTTGGCCCTCACTCA 817  
DB 2153 CACACTAATGTGTGTGGGGGTCTGACTCTCTGAGTCCCTTGGCCCTCACTCA 2202  
QY 818 GGTAGAACCGGAGAGTCTCTGCTCCCGCTCAGACACTAGAACTTTCCAAAGAAATAGGA 877  
DB 2203 GGTAGAGGCCAAGAGATCTCTGCT-CCCCACTCAGAGACTGAACTTTCCAAAGAAATAGGA 2261  
QY 878 GATTATCCCAAGTCCCGTGTCCAGGCTGTGTGGGTTCTGTCTCTCTCCACCC 937  
DB 2262 GATTATCCCAAGTCTGTGTCCAGGCTGTGTGGGTTCTGTCTCTCTCCACCC 2321  
QY 938 CAGTATCTGTGATCTTGAAGATGGTGCACATCCAGTGTCTGTGGAGTGTCCATGAG 997  
DB 2322 CAGTATCTGTGATCTTGAAGATGGTGTGACAT--GGGTCTGTGGGTTTCCATGAG 2379  
QY 998 AGATGCAAAAGTCTTGAATTTTCTGACTTCTCTTTCAGACCCGCCCAAGACACAGCTGA 1057  
DB 2380 GAGTGCAAAAGTCTGAAATTTTCTGACTTTC--TCAGATCTTCCAAAGGACACAGCTTG 2436  
QY 1058 CCCACACCCCTGTCTTTGACTATAGGCGCACCCCTGAGAGTGTGTGGGCTCTTAC 1117  
DB 2437 CCCACACCCCTGTCTTGCACATGAGGCGCACCCCTGAGAGTGTGTGGGCTCTTAC 2496  
QY 1118 CTGGGAGATCATACTGACTGCGAGCGGATGGGAGAGACCAAGCCAGAGCTGGAGC 1177  
DB 2497 CTGGGAGATCATACTGACTGCGAGCGGATGGGAGAGACCAAGCCAGAGCTGGAGC 2556  
QY 1178 TCGTGGAGACAGGCTCTGAGGGATGGAACCTTTCAGAACTGGGCGACTGTGTGTGTC 1237  
DB 2557 TTTGTTGAGACAGGCTCTGAGGGATGGAACCTTTCAGAACTGGGCGACTGTGTGTGTC 2616  
QY 1238 CTTCGGAGAGAGACGAGATACAGTGTCCAGTGTCCAGAGAGGGGCTGCGGAGGCC 1297  
DB 2617 CTTCGGAGAGAGACGAGATACAGTGTCCAGTGTCCAGAGAGGGGCTGCGGAGGCC 2676  
QY 1298 TCACTGATGATGAGTAAAGAGGAGAT-----GAGGATCATGT 1339  
DB 2677 TCACTGATGATGAGTAAAGAGGAGATGGTAAAGAGGAGAGAGGCTCATGTCT 2736  
QY 1340 CTGTTAGGGAAGACAGAGCTCTGTGAAGACCTTAAACAGGTTGGTGTGAGGCTGG 1399  
DB 2737 TTTCTAGGGAAGACAGAGCTCTGTGAAGCTTAAACAGGTTGGTGTGAGGCTGG 2796  
QY 1400 GGGTACAGAGACCTCAGCTTCACTCTTCCAGAGAGTCTTCCCTGCCACCATCC 1459  
DB 2797 AATACAGGAGCCCTTACCTCTCTTCCAGAGAGTCTTCCAGGCGCCACCATCC 2856  
QY 1460 CATCATGGGTATGTTGTGAGGCTGTGTCTTCCAGAGAGTCTTCCCTGCCACCATCC 1519  
DB 2857 CATCGTGGGATGTTGTGAGGCTGTGTCTTCCAGAGAGTCTTCCCTGCCACCATCC 2916  
QY 1520 CGCTGTGTGTGTGAGAAAGAAAGAGTCAAGTAAAGGGGAGCAAGGGGCTGTG 1579  
DB 2917 CGCTGTGTGTGTGAGAAAGAAAGAGTCAAGTAAAGGGGAGCAAGGGGCTGTG 2975  
QY 1580 AGTTTCTGTCCCACTGGGGGTTTCAAGCCCAAGTAAAGTGTGCTGTGCTGTTAC 1639  
DB 2976 AGTTTCTGTCCCACTGGGGGTTTCAAGCCCAAGTAAAGTGTGCTGTGCTGTTAC 3035  
QY 1640 TGGGAAGACCATCCACTCATATGGGCTTACCCAGCTTGGGCTGTGTGTGCGACACTT 1699  
DB 3036 TGGGAAGACCATCCACTCATATGGGCTTACCCAGCTTGGGCTGTGTGTGCGACACTT 3095  
QY 1700 CTCTTTTGAAGCACTCTGACATGAAGAGACAGATTTATTAATGATGATGTAGTG 1759

```
DB 3096 CTCATTGTTAAAGCTCCTGTGATAAATGAAGACAGATTCTTCACTGAGATATATGCTG 3155
QY 1760 ATG--GGAGCCGATCCCAATATCACAGTCA--GGAGAGTCTCCGCTGAAGACAGA 1816
DB 3156 GTGATGGAGCGATGCCAGGAGTCACAAATCACAGGGGAAGGCTCGCTGATGACAGA 3215
QY 1817 CCTTAGAGAGGCGATTTGGTTCAGAGACCCACATCTGCTTCCCTGTTTCTGATC--GC 1874
DB 3216 CCTCAGAGAGGCGATTTGGTTCAGAGACCCACATCTGCTTCTGATATTTCTGATCTGCG 3275
QY 1875 CCTGGGTTCGACATCACATTTCTGAGAACTTCTCAGGGTCCAAACACTAGAGAGTCC 1934
DB 3276 CCTGATCTACAGTACACTTCTTGGAACCTTCTGAGGATCAAGACTAGGGGTTTCG 3335
QY 1935 TCTAGAGACCTCATGCCCCCTGACCCCTTCTGACCTCTCACAGACATTTCTTCCACAG 1994
DB 3336 TCTAGAGACCTCATGCCCCCTGACCCCTTCTGACCTCTCACAGACATTTCTTCCACAG 3395
QY 1995 ATTGAAAAGGAGGAGCTACTCTCAGGCTGCAAGTATGAGAGAGGCTGATCCCTGA 2054
DB 3396 ATGAAACAGAGGAGGAGCTACTCTCAGGCTGCAAGTATGAGAGAGGCTGATCCCTGA 3454
QY 2055 GATCCTTGGGATCTGTGTTTGGAGGC--ATGGGGAGAGCTACCCACCCACAATTTCTC 2113
DB 3455 GATTTGGGATATTTGTTGGTCAAGAGCTATGAGAGAGCTACCCACCCACAATTTCTC 3514
QY 2114 CTCTGGCCACATCTCTGCTGCTGTGACAGAGTGTGTTTGTCTTACTCTAGAGT 2173
DB 3515 -----TACCACATCTGTGGGCTCTGACAGGTCCTGTTTGTCTTACTCTAGAGT 3568
QY 2174 GACAGTGGCCAGGCTCTAATGTGCTCTCACGGCTTGAATGTGACACCC-----CGG 2228
DB 3569 GACAGTGGCCAGGCTCTGAGGCTGTCTCTCACAGCTAATGAAGTGTGACTCCAGGGCAG 3628
QY 2229 GGGGCTGATGTGTGTGGGTTTGGAGGG---AACAGGGACATPAGCTGTATGAGG 2285
DB 3629 GGGGCTGATGTGTGTGGGTTTGGAGGG---AACAGGGACATPAGCTGTATGAGG 3688
QY 2286 TTTCTTTGACTCATGATTGAGCATGTGATGGGCTTTAAAGTGTGACCCCTGACTG 2345
DB 3689 TTTCTTTGACTCATGATTGAGCATGTGATGGGCTTTAAAGTGTGAGCTGTGACTG 3748
QY 2346 TGAAGTATGATGATTTGTCATGATATTTT--TCTGATGTGAAACAGCTGCCCTGTGT 2404
DB 3749 TGAAGTATGATGATTTGTCATGATATTTTCTATATGATGTGAGACAGCTTCTGTGT 3808
QY 2405 GGGACTGAGTGGCAGATTT 2424
DB 3809 GGGACTGAGTGGCAGATAT 3828

RESULT 13
AA163980
ID AA163980 standard; DNA: 3357 BP.
XX
AC AA163980;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SRO ID NO 352.
XX
DE Human polynucleotide SRO ID NO 352.
XX
KW Human: antirheumatic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; vituicide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; neurotropic;
KW neuroprotective; antidiabetic; hepatotropic; antidiabetic;
KW antineoplastic; antidiabetic; vulnifer; anticonvulsant; antibacterial;
KW antiparasitic; cardiac; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human; ds.
XX
OS Homo sapiens.
XX
PN WO20015308-A2.
```

DR	WPI; 2001-488781/53.					
xx						
Pt	New isolated nucleic acids and polypeptides, useful for diagnosing,					
Pt	treating and/or preventing human diseases and disorders -					
xx						
PS	Disclosure; SEQ ID NO 352; 664bp + Sequence Listing; English.					
xx						
CC	The invention relates to human polymucleotides (AAI63803-AAI64012) and					
CC	the encoded proteins (AAH434497-AAH434600) useful for preventing, treating					
CC	or ameliorating medical conditions e.g. by protein or gene therapy. The					
CC	genes were isolated from a range of human tissues disclosed in the					
CC	specification. The nucleic acids, proteins, antibodies and (ant)agonists					
CC	are useful in the diagnosis, treatment and prevention of: (a) cancer,					
CC	e.g. breast and ovarian cancer and other cancers of the adrenal gland,					
CC	bone, bone marrow, breast, gastrointestinal tract, liver, lung, or					
CC	urogenital; (b) immune disorders e.g. Addison's disease, allergies,					
CC	autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,					
CC	Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative					
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;					
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and					
CC	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal					
CC	and parasitic infections.					
CC	Note: The sequence data for this patent did not form part of the					
CC	printed specification, but was obtained in electronic format directly					
CC	from WIPO at ftp.wipo.int/pub/published_pat_sequences.					
xx						
SQ	Sequence 3357 BP; 647 A; 949 C; 1036 G; 725 T; 0 other:					
	Query Match            58.3%; Score 1423; DB 22; Length 3357;					
	Best Local Similarity    79.3%; Pred. No. 0;					
	Matches 1967; Conservative    0; Mismatches 375; Indels 139; Gaps 18;					
Oy	5	CCCCGAGTCTCGGGTGTCGGATCC-ACCCCGAGGCCGCGGGACC GCCCAGACCTCTAC	63			
Db	601	CCCGAGTCTCCGGGTCCGAGATCCGCCGCCCGAGGCCGCCGAGACCTCTGCAC	660			
Oy	64	CTCGAGAACCCCAAGGGGCCCTTA-----CCAAAATCCCAGC	101			
Db	661	CGCGAGAGCCCCCAAGGCCCGTTTACCCGGTTTTCAITTTACATTGAGGCCAAAATCCCAGC	720			
Oy	102	GGGTGAGTCCGGCGCAGGCGCAGAGCTCGTGGCGGGGCTGACCGAAGGGGTCGACG	161			
Db	721	GGGTTGTGCGGGGCG- GGCGGGGGCTCGGGGAGCGGGGCTGACCGCGGGCGCGGGCCAG	779			
Oy	162	GTTTTCACACCTCCACATGATGATTTGGCTCGCACCTGGGGTCCGAGAGAGCTCTCTCC	221			
Db	780	GGTCTCACATCATCCAGAGATGTAACGGTCTCGACGTGGGGCGGAGGGGCTCTCTCC	839			
Oy	222	GCGGTATTAACAGATGCTCATGATGTGACAAGATTACTTCGCTGCAACGAGAGACTGC	281			
Db	840	GCGGATATACAGGACCGCTTACGAGCGGCAGAAATTAATCGCCCTTAACGAGSACTGA	899			
Oy	282	GCTCTGAGCCGACGAGCACTGCGGCTCAGATCTCAGAGCCAAGCTGTGAGGCGGCCA	341			
Db	900	GCTCTGAGCCCGCGGCGACACCGCGCTCAGATCACCAACGCAATGGGAGCGGCC	959			
Oy	342	ATGTGGCTAACAAAGAGAGGCTGACCTGCGGAGGGGACAGCTGGTAGTGGCTCCACAGAT	401			
Db	960	GTTGTGGGAGCGCTGAGAAGCTTACTCTGTGAGAGGCTGTGGCTGTGAATCGCTCGCAGAT	1019			
Oy	402	ACCTGGAGAACGGAGAGATGTCAGCGCGCGGATCCAGGSGGCACTGGGCGGCTC	461			
Db	1020	ACCTGGAGAACGGAGAGAGATGTCAGCGCGCGGATCCAGGSGGCACTGGGCGGCTT	1079			
Oy	462	CCTGATCTCTGTAGACCTCTCAGCTGGGCTCAGCAAGAGAGGAAAAATGGGACG	521			
Db	1080	CCCATCTCTATAAGTTCGCGGGGATGGCTCCACAGAGAGAGGAGAAATGGGATC	1139			
Oy	522	AACACTAGAAATATGCGCTCTCTGTGATCTGTAGGAGAGAAATCTCTGGGTTTCCAG	581			
Db	1140	AGCGCTAGATATGTCGCTCTCTGTGAATGAAGAAATGCGATGAGTTTTCGTAGTTTCC--	1197			
Oy	582	ATCCTGTACCAAGACTGATTCTGAGGCGCCGCTCTGCTCTGTGGACAAATTAAGGATG	641			

Db 1198 -----TGTGAGGGGCCCCCTTCTCTCTAGACAACTTAAGGAGT 1237  
 QY AAGTCTGAGGAGTGGAGGGAAGAAATCCCTGGAACATGATGAGGGGTCCCTT 701  
 Db 1238 AGCTCTGAGGAATGGAGGGAAGACAGTCCCTAGAACTGATGAGGGGTCCCTT 1297  
 QY 702 GACCCC-ACAGACGCTT-GGACACAGAGACTTTCCTCAGGCGCTTGTCTGCTCA 759  
 Db 1298 GACCCCTGACAGAGCTTGGAGAACGCTGACTTTCCTCAGGCGCTTGTCTGCTCA 1357  
 QY 760 CACTAATGCTGTGGGGGTGTGACTCCAGTCTCTGATCCCTTGGGCTCCACTCAG 819  
 Db 1358 CACTAGTGTGTGGGGGTGTGACTCCAGTCTCTGATCCCTTGGGCTCCACTCAG 1417  
 QY 820 TCAGAACGAGGTCCTCCGCTCCCGCTCAGAGACTAGAACTTCCAAAGAAATAGAG 879  
 Db 1418 TCAGAGCAGAAAGTCCCTG-TTCCCGCTCAGAGACTCGAACTTCCAAATGATAGAG 1476  
 QY 880 TTATCCAGGTGCCCCGTGTCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939  
 Db 1477 TTATCCAGGTGCCCCGTGTCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1535  
 QY 940 GGTATCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 999  
 Db 1536 GGTGTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1593  
 QY 1000 ATGCAAGTCTTGAATTTTGTGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1059  
 Db 1594 ATGCAAGTCTTGAATTTTGTGACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1653  
 QY 1060 CACCAAGTCTTGTGACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1119  
 Db 1654 CACCAAGTCTTGTGACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1713  
 QY 1120 GCGAGATCATCTGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1179  
 Db 1714 GCGAGATCATCTGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1773  
 QY 1180 GTGGAGACAGGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1239  
 Db 1774 GTGGAGACAGGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1833  
 QY 1240 TCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1299  
 Db 1834 TCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1893  
 QY 1300 ATGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1357  
 Db 1894 ACCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1953  
 QY 1358 GCTCTGTGAAGACCTTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1417  
 Db 1954 GCTCTGTGAAGACCTTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1982  
 QY 1418 TTACCTCTCTTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1477  
 Db 1983 TTACCTCTCTTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2042  
 QY 1478 TGGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1537  
 Db 2043 TGGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2102  
 QY 1538 AAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1597  
 Db 2103 AAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2162  
 QY 1598 GGGGTTTCAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1657  
 Db 2163 GGGGTTTCAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2222  
 QY 1658 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1716

Db 2223 --CAAGGCTTAACGACGCTGGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280  
 QY 1717 TGTGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1776  
 Db 2281 TGTGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340  
 QY 1777 GTATTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1836  
 Db 2341 GCATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2399  
 QY 1837 GAGGACCCAGATCTGT 1896  
 Db 2400 CAGGACCCAGATCTGT 2459  
 QY 1897 TGTGAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1956  
 Db 2460 TGTGAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2519  
 QY 1957 ACCTTCTGCGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2016  
 Db 2520 TCTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2579  
 QY 2017 TCAGGCTGCAAGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2076  
 Db 2580 TCAGGCTGCGTAAAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2605  
 QY 2077 GAGG 2136  
 Db 2606 GAGG 2664  
 QY 2137 TCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2196  
 Db 2665 TCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2724  
 QY 2197 GTCTCTCAGGCTGTGAAATGTGACACC-----CGGGGCGCTGATGTG 2243  
 Db 2725 GTCTCTCAGGCTGTGAAATGTGACACC-----CGGGGCGCTGATGTG 2784  
 QY 2244 TGGGTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2303  
 Db 2785 TGGGTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2844  
 QY 2304 ATGAGCATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2363  
 Db 2845 ATGAGCATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2904  
 QY 2364 TCATGAATAT--TTTCTGTAGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2421  
 Db 2905 TCATGAATAT--TTTCTGTAGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2964  
 QY 2422 TTTGTTCATGCTTCCCTTG 2442  
 Db 2965 TTTGTTCATGCTTCCCTTG 2985  
 RESULT 14  
 AA163979  
 ID AA163979 standard; DNA: 3372 BP.  
 XX  
 AA163979;  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polynucleotide SFO ID NO 351.  
 XX  
 Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
 cerebrioprotective; nootropic; neuroprotective; antibacterial; virucide;  
 fungicide; ophthalmological; cytosolic; immunosuppressive; nootropic;  
 neuroprotective; antidiabetic; hepatotropic; antidiabetic;  
 antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;  
 antiparasitic; cardant; gene therapy; cancer; immune disorder;  
 cardiovascular disorder; neurological disease; infection; human; ds.  
 KW

OS Homo sapiens.  
XX  
PN WO200155308-A2.  
XX  
PD 02-AUG-2001.  
PF  
XX 17-JAN-2001; 2001WO-US01309.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0230963.  
PR 26-JUL-2000; 2000US-0230964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 14-AUG-2000; 2000US-0226279.  
PR 18-AUG-2000; 2000US-0226281.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0228287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239345.  
PR 13-OCT-2000; 2000US-0239337.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-024617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249267.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250191.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;  
XX WPI: 2001-488781/53.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
XX treating and/or preventing human diseases and disorders -  
XX  
XX Disclosure: SEQ ID NO 351: 664bp + Sequence Listing: English.

XX The invention relates to human polynucleotides (AA163803-AA164012) and  
XX the encoded proteins (AA434497-AA43660) useful for preventing, treating  
XX or ameliorating medical conditions e.g. by protein or gene therapy. The  
XX genes were isolated from a range of human tissues disclosed in the  
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists  
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,  
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
XX urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
XX autoimmune hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,  
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
XX colitis; (c) cardiovascular disorders such as myocardial ischaemia;  
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
XX and parasitic infections.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

XX Sequence 3372 BP: 663 A; 961 C; 1024 G; 724 T; 0 other;

Query Match 58.2%; Score 1420.6; DB 22; Length 3372;  
Best Local Similarity 79.2%; Pred. No. 0;

Matches 1966; Conservative 0; Mismatches 399; Indels 116; Gaps 19;

QY 5 CCCGAGTCGCGGCTGTGGATCCACCCGCGCGGACCCGCCACCCCTCTACC 64  
Db CCCAGTCCTCCGCTGTGATGATCCACCCGCGGCTGTGGATCCACCCCTCTACC 653  
QY 65 TGGAGAACCCCAAGGCGCTTTA-----CCAAATCCCGCGG 102  
Db TGGAGAACCCCAAGGCGCTTTA-----CCAAATCCCGCGG 713  
QY 103 GGTGGTCGCGGAGGAGGCTGCTGGGCGGCGGCTGACCGAGGGGTGAGGCGCAG 162  
Db GGTGGTCGCGGAGGAGGCTGCTGGGCGGCGGCTGACCGAGGGGTGAGGCGCAG 773  
QY 163 TTCTCACACCTCCAGTGTGATGTGGCTGCGACCTGGGCTCGACGAGGCTCTCGG 222  
Db TTCTCACACCTCCAGTGTGATGTGGCTGCGACCTGGGCTCGACGAGGCTCTCGG 833  
QY 223 CGGATATGACAGTATGCTACGATGGCAAGATTTACTTCGCTTGAACGAGGACTGCG 282  
Db CGGATATGACAGTATGCTACGATGGCAAGATTTACTTCGCTTGAACGAGGACTGCG 893  
QY 283 CTCTTGACCGCAGGACGACTGGGCTGAGTCTCCAAAGCAGTGTGAGGCGCCAA 342  
Db CTCTTGACCGCAGGACGACTGGGCTGAGTCTCCAAAGCAGTGTGAGGCGCCAA 953  
QY 343 TGTGAGTGAACAAAGAGAGCTTACCTGAGGAGGACGTGGAGTGTGCTCCACAGATA 402  
Db TGTGAGTGAACAAAGAGAGCTTACCTGAGGAGGACGTGGAGTGTGCTCCACAGATA 1013  
QY 403 CCTGAGAGAGGAGAGAGATGCTGACGCGCGGCTTACAGGAGGAGTGGGCGCTTCC 462  
Db CCTGAGAGAGGAGAGAGATGCTGACGCGCGGCTTACAGGAGGAGTGGGCGCTTCC 1073  
QY 463 CTGATCTCTCTAAGTCTCTACAGCTGCTTACACAGAGAGAGGAGAAATGGAGCA 522  
Db CTGATCTCTCTAAGTCTCTACAGCTGCTTACACAGAGAGAGGAGAAATGGAGCA 1133  
QY 523 AACTAGAAATATGCGCTCCCTGCTGCTGAGGAGAGAGAAATCCCTCGGCTTTCAGA 582  
Db AACTAGAAATATGCGCTCCCTGCTGCTGAGGAGAGAGAAATCCCTCGGCTTTCAGA

Db 1134 GCGCTGGAATATGCGCTCCCTGCTGCTGAGTGAATGGAGATGCTTCTGAGTTTC---- 1189  
QY 583 TCTGTACAGAGAGTATGATGTGAGGGCCGCTGCTGCTGCTGAGCAATTAAGGATGA 642  
Db 1190 -----TTCTGAGGGCCCGCTGCTGCTGCTGCTGAGCAATTAAGGATGA 1231  
QY 643 AGTCTGAGGAGTGGAGGAGAGCAATTCCTGAGAGCTGATCAGGGTTCCTTTTG 702  
Db 1232 AGTCTGAGGAGTGGAGGAGAGCAATTCCTGAGAGCTGATCAGGGTTCCTTTTG 1291  
QY 703 ACC-----CCACAGAGCTTGGACAGGAGCTTTCCTCCCGCAGGCTTTGT 749  
Db 1292 ACCACTTGGACAGCTGAGGAGAGTGTGCTGAGGCTGCTGCTGCTGAGCTTTGT 1351  
QY 750 CTGTGCTCAGCTCAATGTGTGAGGGCTGCTGAGCTGCTGCTGAGTCTGAGTCTTGGCC 809  
Db 1352 CTGTGCTCAGCTCAATGTGTGAGGGCTGCTGAGCTGCTGAGTCTGAGTCTTGGCC 1411  
QY 810 TCCACTGAGTGAAGAGGAGTCCCTGCTCCCGCTGAGAGCTGAGAACTTCCAG 869  
Db 1412 TCCACTGAGTGAAGAGGAGTCCCTGCTCCCGCTGAGAGCTGAGAACTTCCAG 1470  
QY 870 GAATAGAGATTAATCCAGAGTCCCTGCTGAGAGCTGCTGAGTCTGAGTCTTGGCTT 929  
Db 1471 GAATAGAGATTAATCCAGAGTCCCTGCTGAGAGCTGCTGAGTCTGAGTCTTGGCTT 1530  
QY 930 CCCGACCCGAGTATGCTTATTTAGATGCTGATCAGTCTGCTGAGTCTGCTGAGTGT 989  
Db 1531 CCCGACCCGAGTATGCTTATTTAGATGCTGATCAGTCTGCTGAGTCTGCTGAGTGT 1588  
QY 990 CCGATGAGATTAATCCAGAGTCCCTGCTGAGAGCTGCTGAGTCTGAGTCTTGGCTT 1049  
Db 1589 CCGATGAGATTAATCCAGAGTCCCTGCTGAGAGCTGCTGAGTCTGAGTCTTGGCTT 1648  
QY 1050 ACAGTGTACCCAGTCTGCTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1109  
Db 1649 ACAGTGTACCCAGTCTGCTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1708  
QY 1110 CTCTTACCTGCGGAGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1159  
Db 1709 CTCTTACCTGCGGAGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1768  
QY 1170 CGTGGAGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1229  
Db 1769 CGTGGAGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1828  
QY 1230 GGTGGTCCCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1289  
Db 1829 GGTGGTCCCTTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1888  
QY 1290 GAGAGCCCTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1349  
Db 1889 GAGAGCCCTGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1947  
QY 1350 AAGCAGAGGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1409  
Db 1948 AAGCAGAGGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2007  
QY 1410 CCGTACCTTACCTGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1469  
Db 2008 CCGTACCTTACCTGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2067  
QY 1470 ATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1526  
Db 2068 ATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2127  
QY 1527 GTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1586  
Db 2128 GTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2187  
QY 1587 TTGCTCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1646  
Db 2188 TTGCTCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2246







523 ACACTAGATATGCCCCCTCCCTCTGCTCTGAGGAGAGAAATCCTCTGGGTTTCCAGA 582  
1134 GCGGTGAATATGCCCCCTCCCTGAAATGGAATGGATGAGTTTCTCGAATTTTC---- 1189  
583 TCTGTATCCAGAGAGTATTTCTGAGGGCCCTCCCTCTCTGAGCAATTAAGGATGA 642  
1190 -----TTCTGAGGGCCCCCTCTCTCTCTAGAGCAATTAAGGATGA 1231  
643 AGTCTGTAGGAGAGGGGGAAGCAATCCCTGGAGAGCTGATCAGGGGTTCCCTTGG 702  
1232 AGTCTGTAGGAGAGGGGGAAGCAATCCCTGGAGAGCTGATCAGGGGTTCCCTTGG 1291  
703 ACC-----CCACAGACGCTTGGACACAGAGCTTTCCCTCAGGCTTGT 749  
1292 ACCATTGTGACCACTGACAGAGCTGTGGCTGTGACCTTCTCTCAGGCTTGT 1351  
750 CTCTGCTGACACATGATGTTGTGGGGTGTGACTGACCTCTCTGAGTCCCTTGGGC 809  
1352 CTCTGCTGACAGCTCAATGTTTAAAGTTTGAATTCCAACTTTCTGAGTCCCTTGGGC 1411  
810 TCCACTGAGTCAAGACCGAGAGTCCCTGCTCCCGCTCAGAGACTAGAACTTTCCAA 869  
1412 TCCACTGAGTCAAGACCGAGAGTCCCTGCTCCCGCTCAGAGACTAGAACTTTCCAA 1470  
870 GAATGAGAGATTAATCCAGAGTCCCTGCTCCCGCTCAGAGACTAGAACTTTCCAA 929  
1471 GAATGAGAGATTAATCCAGAGTCCCTGCTCCCGCTCAGAGACTAGAACTTTCCAA 1530  
930 CCCCACCCAGATATGCTGCTTCTTGAAGATGTCACATCCAGAGTCTGCTGAGAT 989  
1531 CCCCACCCAGATATGCTGCTTCTTGAAGATGTCACATCCAGAGTCTGCTGAGAT 1588  
990 CCCCAGAGATGACAAAGTCTGATTTCTGACTCTTCTTCTGAGACCCCTTCCAA 1049  
1589 CCCCAGAGATGACAAAGTCTGATTTCTGACTCTTCTTCTGAGACCCCTTCCAA 1648  
1050 ACAGTGAAGACCAACCTGCTTCTGACTATGAGGACCACTTGAAGTGGGCTGGG 1109  
1649 ACAGTGAAGACCAACCTGCTTCTGACTATGAGGACCACTTGAAGTGGGCTGGG 1708  
1110 CTTTACCTGCGGAGATCATACTGACCTGACGCGGAGTGGGAGGACCAAGCCAG 1169  
1709 CTTTACCTGCGGAGATCATACTGACCTGACGCGGAGTGGGAGGACCAAGCCAG 1768  
1170 CCGTGAAGTCTGAGAGACCAAGGCTGACGCGGAGTGGGAGGACCAAGCCAG 1229  
1769 CACCGAGCTTGTGAGAGACCAAGGCTGACGCGGAGTGGGAGGACCAAGCCAG 1828  
1230 GGTGAGCTTCTGAGAGAGAGATACACGCTGATGAGAGTGAAGGGCTGCC 1289  
1829 GGTGAGCTTCTGAGAGAGAGATACACGCTGATGAGAGTGAAGGGCTGCC 1888  
1290 GAGAGCCCTCATGAGAGTGAAGAGGAGAGTGAAGAGTGAAGAGTGAAGAG 1349  
1889 GAGAGCCCTCATGAGAGTGAAGAGGAGAGTGAAGAGTGAAGAGTGAAGAG 1947  
1350 AACGAGAGCTCTGAGAGCTTGAAGAGTGAAGAGGAGTGAAGAGTGAAGAG 1409  
1948 GGAAGAGAGAGTCTGAGAGCTTGAAGAGGAGTGAAGAGTGAAGAGTGAAGAG 2007  
1410 CCGTCACTTCAACCTCTTCCAGAGAGTCTTCCCTGACCAACATCCCATGAGGT 1469  
2008 CCGTCACTTCCCTCTTCCAGAGGACATCTTCCAGAGGACCAACATCCCATGAGGT 2067  
1470 ATGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1526  
2068 ATGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2127  
1527 GTGCTGTGAGAGAGAGTCAAGTGAAGAGGAGTGAAGAGTGAAGAGTGAAGAG 1586  
2128 GTGCTGTGAGAGAGAGTCAAGTGAAGAGGAGTGAAGAGTGAAGAGTGAAGAG 2187

1587 TTGTCACACAGGGGTTTCAAGCCACAGGAGAGAGTGTCCCTGCTGTTACTGGAG 1646  
2188 TTGTCACACAGGGGTTTCAAGCCACAGGAGAGAGTGTCCCTGCTGTTACT--GAGAG 2246  
1647 CACCATCCACATCATAGGGCTTACCAAGCTGGG--CCTGTGTGACAGACCTTCTT 1705  
2247 CACCATCCACA--CATGGGCTATCCAGGCTGGAGCCCTGTGTGAGCACTTACTGT 2304  
1706 TGTAAACACCTGTGAGCAATGAAGAGACAGATTAATACCTGATGATGATGATGATG 1765  
2305 TGTAAACAC--ATGACAAATGAAGAGACAGATTAATACCTGATGATGATGATGATG 2362  
1766 ACC--TGATCCAGTAAATCAGAGTCAAGAGAGAGTCCCTGCTGAGAGACAGACTT 1824  
2363 TCTGATTAATCAGAGTCAATGAGTCAAGAGAGTCCCT--GCTAAGGACAGACTT 2421  
1825 GGGCAGTTGGTCAAGACCAACATGCTTCTTCTGTTTCTGATGATGATGATGATG 1884  
2422 GGGCAGTTGGTCAAGACCAACATGCTTCTTCTGTTTCTGATGATGATGATGATG 2481  
1885 CAGTCAACATTTCTGGAACCTTCTGAGGGTCCAGAGTCAAGAGAGTCTCTGAGAGCT 1944  
2482 TCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2541  
1945 CATGACCTGCTGACCTTCTGAGCTTCAAGAGACATTTTCTTCCAGAGATGAAGAG 2004  
2542 CATGACCTGCTGACCTTCTGAGCTTCAAGAGACATTTTCTTCCAGAGATGAAGAG 2601  
2005 AGGAGTACTTCTGAGCTGCAATGATGATGAAGAGAGTGAATCCCTGAGATCCTGG 2064  
2602 AGGAGTACTTCTGAGCTGCAATGATGATGAAGAGAGTGAATCCCTGAGATCCTGG 2646  
2065 ATCTGTGTTGGAGGACATGAGGAGCTCACACCCACCAATTCCTCTGAGGACAG 2124  
2647 -----TGAAGAGCTCACACCCCAATTCCTCTGAGGACAG 2686  
2125 TCTGCTGATGCTGACCAAGT--GCTGTTTCTTCTTCTGATGATGATGATGATGATG 2183  
2687 TCTGCTGATGCTGACCAAGT--GCTGTTTCTTCTTCTGATGATGATGATGATGATG 2746  
2184 AGGAGTACTTCTGAGCTGCAATGATGATGAAGAGAGTGAATCCCTGAGATCCTGG 2243  
2747 AGGAGTACTTCTGAGCTGCAATGATGATGAAGAGAGTGAATCCCTGAGATCCTGG 2801  
2244 TGGGTTTGAAGAGAGAGGAGATGCTGTGATGAGGTTTCTTCTGATGATGATGATG 2303  
2802 TGGGTTTGAAGAGAGAGGAGATGCTGTGATGAGGTTTCTTCTGATGATGATGATG 2861  
2304 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2363  
2862 TGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2921  
2364 TGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2421  
2922 TGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2980  
2422 TTTGTTCAATGCTTCTTCTG 2442  
2981 TTTCTTCAACATTTCTTCTG 3001

Search completed: January 30, 2003, 22:22:36  
Job time : 798 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:09:14 ; Search time 4763 Seconds  
(without alignments)  
12836.704 Million cell updates/sec

Title: US-09-622-846-16  
Perfect score: 2442  
Sequence: 1 tactcccgagctccggytc.....tgytcatgcttccttgy 2442

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues  
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

```
1: /cgn2_6/ptodata/2/pna/PCRUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US095_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095T_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
```

44: /cgn2\_6/ptodata/2/pna/US600\_COMB.seq:\*  
45: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*  
46: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*  
47: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*  
48: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*  
49: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*  
50: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*  
51: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*  
52: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*  
53: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*  
54: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*  
55: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*  
56: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*  
57: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*  
58: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*  
59: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*  
60: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*  
61: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*  
62: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*  
63: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*  
64: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*  
65: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*  
66: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*  
67: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq:\*  
68: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*  
69: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*  
70: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*  
71: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*  
72: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*  
73: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*  
74: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*  
75: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*  
76: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*  
77: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*  
78: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*  
79: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*  
80: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq:\*  
81: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*  
82: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq:\*  
83: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq:\*  
84: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*  
85: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	2442	100.0	2442	24	US-09-622-846-16	Sequence 16, Appl
2	2440.4	99.9	2441	24	US-09-622-846-17	Sequence 17, Appl
3	2420	99.1	2442	24	US-09-622-846-18	Sequence 18, Appl
4	2418.4	99.0	2441	24	US-09-622-846-19	Sequence 19, Appl
5	1768.4	72.4	4465	17	US-09-359-922-598	Sequence 598, App
6	1768.4	72.4	4465	17	US-09-359-922-598	Sequence 598, App
7	1768.4	72.4	4465	34	US-09-919-002-598	Sequence 598, App
8	1694.4	69.4	4000	40	US-10-102-524-1722	Sequence 1722, Ap
9	1694.4	67.5	5030	33	US-09-881-797-3560	Sequence 3590, Ap
10	1648.2	67.5	5030	38	US-10-021-698-3550	Sequence 3590, Ap
11	1648.2	67.5	5030	38	PCT-US01-01328-573	Sequence 573, App
12	1554	63.6	3098	1	PCT-US01-01328A-573	Sequence 573, App
13	1554	63.6	3098	1	PCT-US01-01334-10456	Sequence 10456, A
14	1554	63.6	3098	1	PCT-US01-01339-6712	Sequence 6712, Ap
15	1554	63.6	3098	1	PCT-US01-01354-41683	Sequence 41683, A
16	1554	63.6	3098	1	PCT-US01-01354-41683	Sequence 41683, A
17	1554	63.6	3098	30	US-09-764-874-10456	Sequence 6712, Ap
18	1554	63.6	3098	30	US-09-764-891-6712	Sequence 6712, Ap
19	1554	63.6	3098	36	US-09-764-905-41683	Sequence 5612, Ap
20	1554	63.6	3098	36	US-09-950-083-5612	Sequence 6415, Ap
21	1554	63.6	3098	36	US-09-950-083-6415	Sequence 6415, Ap

```

22 1554 63.6 3098 36 US-09-950-083-6779 Sequence 6779, Ap
23 1554 63.6 3098 36 US-09-950-083-9747 Sequence 9747, Ap
24 1554 63.6 3098 39 US-10-091-572-573 Sequence 573, App
25 1554 63.6 3098 39 US-10-092-399-41683 Sequence 41683, A
26 1554 63.6 3098 39 US-10-092-400-10456 Sequence 10456, A
27 1554 63.6 3098 40 US-10-105-299-7673 Sequence 7673, Ap
28 1554 63.6 3098 40 US-10-105-299-8566 Sequence 8566, Ap
29 1554 63.6 3098 40 US-10-105-299-8930 Sequence 8930, Ap
30 1554 63.6 3098 40 US-10-105-299-11898 Sequence 11898, A
31 1551.6 63.5 4316 33 US-09-880-107-3713 Sequence 3713, Ap
32 1444.6 59.2 3520 16 US-09-220-132-84 Sequence 84, App1
33 1444.6 59.2 3520 41 US-10-155-653-84 Sequence 84, App1
34 1439.6 59.0 3840 36 US-09-971-429B-10 Sequence 10, App1
35 1431.2 58.6 32768 65 US-60-213-178-223 Sequence 223, App
36 1423 58.3 3357 1 PCT-US01-01309-352 Sequence 352, App
37 1423 58.3 3357 1 PCT-US02-09188-1621 Sequence 1621, Ap
38 1423 58.3 3357 1 PCT-US02-09370-1713 Sequence 1713, Ap
39 1423 58.3 3357 1 PCT-US02-09922-1059 Sequence 1059, Ap
40 1423 58.3 3357 36 US-09-950-082-2079 Sequence 2079, Ap
41 1423 58.3 3357 40 US-10-105-289-7273 Sequence 7273, Ap
42 1423 58.3 3357 41 US-10-158-057-352 Sequence 352, App
43 1420.6 58.2 3372 1 PCT-US01-01309-351 Sequence 351, App
44 1420.6 58.2 3372 1 PCT-US01-01309-383 Sequence 383, App
45 1420.6 58.2 3372 41 US-10-158-057-351 Sequence 351, App

```

## ALIGNMENTS

```

RESULT 1
US-09-622-846-16
: Sequence 16, Application US/09622846
: GENERAL INFORMATION:
: APPLICANT: National University of Ireland, Cork
: TITLE OF INVENTION: HIV Linked Pre-Exposure and Miscarriage Susceptibility
: FILE REFERENCE: P197/PCT
: CURRENT APPLICATION NUMBER: US/09/622, 846
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: IE980134
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: IE980668
: PRIOR FILING DATE: 1998-08-12
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 16
: LENGTH: 2442
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-622-846-16

```

```

Query Match 100.0%; Score 2442; DB 24; Length 2442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TACCTCCGAGTCGCGGTCGAGATCCACCCGAGGCGCGGAGCCCGCAGACCTTC 60
Db 1 TACTCCGAGTCGCGGTCGAGATCCACCCGAGGCGCGGAGCCCGCAGACCTTC 60
QY 61 TACCTGGAGAACCCCAAGCGCCCTTACCAAAATCCCGCGGTCGTCGCGGCGAGG 120
Db 61 TACCTGGAGAACCCCAAGCGCCCTTACCAAAATCCCGCGGTCGTCGCGGCGAGG 120
QY 121 CGAGGCTCGGTCGCGGTCGAGCCGAGGCGGTCGTCGAGACCTTCGAGG 180
Db 121 CGAGGCTCGGTCGCGGTCGAGCCGAGGCGGTCGTCGAGACCTTCGAGG 180
QY 181 GATGATTCGTCGACCTTCGAGTCGAGGAGCCCTTCCTCCGCGGTCATGACATGATTC 240
Db 181 GATGATTCGTCGACCTTCGAGTCGAGGAGCCCTTCCTCCGCGGTCATGACATGATTC 240
QY 241 CTAGATGGCAGAGATTACTCTCCCTGAGCAGAGACCTTCCTCTGAGCCGAGCGA 300
Db 241 CTAGATGGCAGAGATTACTCTCCCTGAGCAGAGACCTTCCTCTGAGCCGAGCGA 300

```

```

Db 241 CTACGATGCAAGGATTTACTCTGCGCCCTGAAAGAGACCTGCGCTCCGAGCCGAGCGA 300
QY 301 CACGCGGCTCAGATCTCCCAAGGCAAGTGTGAGGCGGCAATGTGGTGAACAAAGAG 360
Db 301 CACGCGGCTCAGATCTCCCAAGGCAAGTGTGAGGCGGCAATGTGGTGAACAAAGAG 360
QY 361 AGCTTACCTGGAGGCAAGTGTGAGTGTCCAGATACCTGGAGACGAGGAGGA 420
Db 361 AGCTTACCTGGAGGCAAGTGTGAGTGTCCAGATACCTGGAGACGAGGAGGA 420
QY 421 GATGCTCAGCGCGCGGTCACAGGCGCAATGGGCGCTCCCTATCTCTGAGACT 480
Db 421 GATGCTCAGCGCGCGGTCACAGGCGCAATGGGCGCTCCCTATCTCTGAGACT 480
QY 481 CTCAGCTGCGCTGAGCAGCAGAGAGAGGAAATGGACCAACCTACATATGCGCT 540
Db 481 CTCAGCTGCGCTGAGCAGCAGAGAGAGGAAATGGACCAACCTACATATGCGCT 540
QY 541 CCCCTGCTGCTGAGGAGAGGAAATCTCTGCTGCTTCCAGATCCGTAACAGAGTGA 600
Db 541 CCCCTGCTGCTGAGGAGAGGAAATCTCTGCTGCTTCCAGATCCGTAACAGAGTGA 600
QY 601 TTCTGAGGCGCGCTCTGCTCTCTGAGACATTAAGGATGAATCTGAGGAGTGA 660
Db 601 TTCTGAGGCGCGCTCTGCTCTCTGAGACATTAAGGATGAATCTGAGGAGTGA 660
QY 661 GGGGAAACAAATCCCTGGAGAGACTGATCAGGGTTCCTTTGACCCACAGACTCTGG 720
Db 661 GGGGAAACAAATCCCTGGAGAGACTGATCAGGGTTCCTTTGACCCACAGACTCTGG 720
QY 721 CACGAGACTTTTCCCTCAGGCTTGTCTGCTGCTCAGCTCAGCTCATGTGTGGGCTC 780
Db 721 CACGAGACTTTTCCCTCAGGCTTGTCTGCTGCTCAGCTCAGCTCATGTGTGGGCTC 780
QY 781 TGAATCAGTCTCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTG 840
Db 781 TGAATCAGTCTCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTG 840
QY 841 CCCCGCTCAGAGACTGAACTTTCCAGAGAAATGAGATTTCCAGAGTCCCTGCTC 900
Db 841 CCCCGCTCAGAGACTGAACTTTCCAGAGAAATGAGATTTCCAGAGTCCCTGCTC 900
QY 901 AGGCTGCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGGCTGCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 961 ATGCTACATCCAGTGTCTGAGTCCCTGAGTCCCTGAGATCCCAAGATCAAAAGTTTC 1020
Db 961 ATGCTACATCCAGTGTCTGAGTCCCTGAGTCCCTGAGATCCCAAGATCAAAAGTTTC 1020
QY 1021 TGACTCTTCTTTCAGACCCCGCCAGACACAGTACACCCAGCTCTCTTACAT 1080
Db 1021 TGACTCTTCTTTCAGACCCCGCCAGACACAGTACACCCAGCTCTCTTACAT 1080
QY 1081 GAGGCAACCTGAGTGTCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGT 1140
Db 1081 GAGGCAACCTGAGTGTCTGAGTCCCTGAGTCCCTGAGTCCCTGAGTCCCTGAGT 1140
QY 1141 CAGCGGATGGGAGAGACCAAGCCAGAGAGTGTGAGTGTGAGAGCAGGCTCAGG 1200
Db 1141 CAGCGGATGGGAGAGACCAAGCCAGAGAGTGTGAGTGTGAGAGCAGGCTCAGG 1200
QY 1201 GATGAACTTCCAGAGTGGGAGGCTGAGTGTGAGTGTGAGTGTGAGAGAGAGATAC 1260
Db 1201 GATGAACTTCCAGAGTGGGAGGCTGAGTGTGAGTGTGAGTGTGAGAGAGAGATAC 1260
QY 1261 AGTGCATGTGAGAGTGAAGGAGGCTGCGGAGCCCTCATCTGATGAGTGAAGAG 1320
Db 1261 AGTGCATGTGAGAGTGAAGGAGGCTGCGGAGCCCTCATCTGATGAGTGAAGAG 1320
QY 1321 GGAATGAGAGGATCATGTCTGTTAGGAAAGCAGAGAGCTCTGAGAGACCTTTAAG 1380
Db 1321 GGAATGAGAGGATCATGTCTGTTAGGAAAGCAGAGAGCTCTGAGAGACCTTTAAG 1380

```





Db 661 GGGGAGACAAATCCCTGGAAGACTGATCAAGGGTCCCTTTGACCCACAGACGCTTGG 720  
 QY 721 CACGAGAGATTTTCCCTAGGCTTGTCTCTGCTCAACACATATGTGTGGGGGTC 780  
 Db 721 CACGAGAGATTTTCCCTAGGCTTGTCTCTGCTCAACACATATGTGTGGGGGTC 780  
 QY 781 TGACTCCAGCTCCTCTGAGTCCCTTGGCCCTCACTAGCTCAGAACCGAGGTCCCTGCT 840  
 Db 781 TGACTCCAGCTCCTCTGAGTCCCTTGGCCCTCACTAGCTCAGAACCGAGGTCCCTGCT 840  
 QY 841 CCCCCCTCAGAGACTGAACTTCCAGAGATAGAGATTAATCCAGGTGCCGCTGTC 900  
 Db 841 CCCCCCTCAGAGACTGAACTTCCAGAGATAGAGATTAATCCAGGTGCCGCTGTC 900  
 QY 901 AGGCTGTGTCTGGTCTGTCTGCTCCCTTCCACCCAGGTATCTGTTCTTTAGG 960  
 Db 901 AGGCTGTGTCTGGTCTGTCTGCTCCCTTCCACCCAGGTATCTGTTCTTTAGG 960  
 QY 961 ATGCTCAATCCAGGCTGCTGAGAGTCCATGAGAGATGCAAGTGTGAATTTTC 1020  
 Db 961 ATGCTCAATCCAGGCTGCTGAGAGTCCATGAGAGATGCAAGTGTGAATTTTC 1020  
 QY 1021 TGACTCTTCTTTCAGACCCCCCAAGACACACAGTACCCACCTCTTTGACTAT 1080  
 Db 1021 TGACTCTTCTTTCAGACCCCCCAAGACACACAGTACCCACCTCTTTGACTAT 1080  
 QY 1081 GAGGCTACCCCTGAGAGTCCCTGGGCTGCTGCTACCTGGGAGATCTACTGACTGG 1140  
 Db 1081 GAGGCTACCCCTGAGAGTCCCTGGGCTGCTGCTACCTGGGAGATCTACTGACTGG 1140  
 QY 1141 CACCGGAGATGGGAGACACAGACCCAGAGAGTGTGAGAGACAGGCTGTGAGG 1200  
 Db 1141 CACCGGAGATGGGAGACACAGACCCAGAGAGTGTGAGAGACAGGCTGTGAGG 1200  
 QY 1201 GATGAGACCTTCCAGAGTGGGAGAGTGTGCTGCTCTTCTGAGAGAGAGAGATTC 1260  
 Db 1201 GATGAGACCTTCCAGAGTGGGAGAGTGTGCTGCTCTTCTGAGAGAGAGAGATTC 1260  
 QY 1261 ACCTGACATGTGACAGATGAGGGGCTGCCGAGCCCTCATGCTGAGATGAGTAAAGAG 1320  
 Db 1261 ACCTGACATGTGACAGATGAGGGGCTGCCGAGCCCTCATGCTGAGATGAGTAAAGAG 1320  
 QY 1321 GGAATATGAGGAGCATATGTGTGTTAGGAAAGAGAGAGCTCTGTGAACCTTTAAACG 1380  
 Db 1321 GGAATATGAGGAGCATATGTGTGTTAGGAAAGAGAGAGCTCTGTGAACCTTTAAACG 1380  
 QY 1381 GGTGGTGTGAGAGGCTGGGGGTCAGAGACCTTCACTTCCCTTCCAGAGACT 1440  
 Db 1381 GGTGGTGTGAGAGGCTGGGGGTCAGAGACCTTCACTTCCCTTCCAGAGACT 1440  
 QY 1441 CTTCCCTGCTCCACCATCCCATCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 Db 1441 CTTCCCTGCTCCACCATCCCATCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 QY 1501 TAGTCACATGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 Db 1501 TAGTCACATGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
 QY 1561 GGTGACATGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 Db 1561 GGTGACATGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
 QY 1621 GTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 Db 1621 GTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 1681 CCGTGTGTGACAGACCTTCTTTTGTAAAGACCTGTGTACATATAGAGAGATTTAT 1740  
 Db 1681 CCGTGTGTGACAGACCTTCTTTTGTAAAGACCTGTGTACATATAGAGAGATTTAT 1740  
 QY 1741 TACTGTATGATTTTGTATGATGGGAGCTGATCCAGATATATCAGAGTGAAGAGTTC 1800  
 Db 1741 TACTGTATGATTTTGTATGATGGGAGCTGATCCAGATATATCAGAGTGAAGAGTTC 1800

QY 1801 CTTGCTAAAGAGACACTTAGAGGGGAGTTGTGAGAGACCAACATCTCTTCTTGG 1860  
 Db 1801 CTTGCTAAAGAGACACTTAGAGGGGAGTTGTGAGAGACCAACATCTCTTCTTGG 1860  
 QY 1861 TTTTCTGATGCGCCCTGGGCTGTGAGTACACATTTTCTGGAATCTTCTGAGGTCCTAA 1920  
 Db 1861 TTTTCTGATGCGCCCTGGGCTGTGAGTACACATTTTCTGGAATCTTCTGAGGTCCTAA 1920  
 QY 1921 GACTAGAGGTTCTCTAGAGACCTCATGAGCCCTGACACTTCTGCTCTGCTGCTGCTG 1980  
 Db 1921 GACTAGAGGTTCTCTAGAGACCTCATGAGCCCTGACACTTCTGCTCTGCTGCTGCTG 1980  
 QY 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTATGATGAAG 2040  
 Db 1981 TTTTCTTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTATGATGAAG 2040  
 QY 2041 AGGCTATCCCTGAGATCCCTTGGGATCTTGTGTTGGAGGACCATGAGGAGCTCACCCAC 2100  
 Db 2041 AGGCTATCCCTGAGATCCCTTGGGATCTTGTGTTGGAGGACCATGAGGAGCTCACCCAC 2100  
 QY 2101 CCACAAATTCCTCTCTGCGCACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 Db 2101 CCACAAATTCCTCTCTGCGCACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
 QY 2161 TACTCTAGGAGTACAGAGTCCAGGCTCTAATGCTCTCAGGCTGCTGCTGCTGCTGCTG 2220  
 Db 2161 TACTCTAGGAGTACAGAGTCCAGGCTCTAATGCTCTCAGGCTGCTGCTGCTGCTGCTG 2220  
 QY 2221 CACCCGGGGGCTGATGTGTGGTGTGTTGAGGGAAACAGGGAGATAGCTGTCTA 2280  
 Db 2221 CACCCGGGGGCTGATGTGTGGTGTGTTGAGGGAAACAGGGAGATAGCTGTCTA 2280  
 QY 2281 TGAAGTTCTTCTGACTTCAATGATGATGAGCATGTATGAGGCTGTTAAAGTGTACCCCT 2340  
 Db 2281 TGAAGTTCTTCTGACTTCAATGATGATGAGCATGTATGAGGCTGTTAAAGTGTACCCCT 2340  
 QY 2341 CACTGTACTGATATGAAATTTGTTCAATGAAATTTTCTGTAGTGTGAACAGCTGCTCT 2400  
 Db 2341 CACTGTACTGATATGAAATTTGTTCAATGAAATTTTCTGTAGTGTGAACAGCTGCTCT 2400  
 QY 2401 GTGTGGAGTGTGAGGAGATTTGTTCAATGAAATTTTCTGTAGTGTGAACAGCTGCTCT 2442  
 Db 2401 GTGTGGAGTGTGAGGAGATTTGTTCAATGAAATTTTCTGTAGTGTGAACAGCTGCTCT 2442

RESULT 3  
 US-09-622-846-18  
 : Sequence 18, Application us/09622846  
 : GENERAL INFORMATION:  
 : APPLICANT: National University of Ireland, Cork  
 : TITLE OF INVENTION: HLA Linked Pre-Eclampsia and Miscarriage Susceptibility  
 : TITLE OF INVENTION: Gene  
 : FILE REFERENCE: PL977PCT  
 : CURRENT APPLICATION NUMBER: US/09/622,846  
 : PRIOR APPLICATION NUMBER: IE980134  
 : PRIOR FILING DATE: 1998-02-25  
 : PRIOR APPLICATION NUMBER: IE980668  
 : PRIOR FILING DATE: 1998-08-12  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 18  
 : LENGTH: 2441  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 US-09-622-846-18

Query Match 99.1%; Score 2420; DB 24; Length 2441;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACTCCGAGTCTCCGGGCTGAGGATCAACCCGAGGCGCGGAGACCCAGACCTCTC 60

|||||  
Db 1 TACTCCCGAGCTCTCGGGTCTGGGATCCACCCGAGGCCGGGACCCGGCCAGACCTTC 60  
Qy TACTGGAGAACCCCAAGGCGCCTTACCAAAATCCCGGGGTGGGTCCGGGCGAGG 120  
Db TACTGGAGAACCCCAAGGCGCCTTACCAAAATCCCGGGGTGGGTCCGGGCGAGG 120  
Qy 121 CGAGGCTCGGTGGGCGGGGTGACCGAGGGGGTGGGCCAGGTTCTACACCTCCAGTG 180  
Db CGAGGCTCGGTGGGCGGGGTGACCGAGGGGGTGGGCCAGGTTCTACACCTCCAGTG 180  
Qy 181 GATATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGGGGATGAAAGATATGC 240  
Db GATATTGGCTGCGACCTGGGGTCCGACGAGCGCTCTCCGGGGATGAAAGATATGC 240  
Qy 241 CTACGATGGCAAGGATTACCTGCGCTGAACGAGACCTGCGCTCTGAGACCGAGCGGA 300  
Db CTACGATGGCAAGGATTACCTGCGCTGAACGAGACCTGCGCTCTGAGACCGAGCGGA 300  
Qy 301 CACTGCGGCTCAGATCTCCAAAGCCAAAGTGTGAGGCGGCCAATGTGGCTGAACAAGAG 360  
Db CACTGCGGCTCAGATCTCCAAAGCCAAAGTGTGAGGCGGCCAATGTGGCTGAACAAGAG 360  
Qy 361 AGCCTACTGGAGGCGACGCTGCTGGAGTGGGCTCCACAGATACCGTGAAGCGGAAGGA 420  
Db AGCCTACTGGAGGCGACGCTGCTGGAGTGGGCTCCACAGATACCGTGAAGCGGAAGGA 420  
Qy 421 GATGCTGAGGCGGCGGTACCAAGGGGCAATGGGGCGCTCCGATCTCTGTAGACCT 480  
Db GATGCTGAGGCGGCGGTACCAAGGGGCAATGGGGCGCTCCGATCTCTGTAGACCT 480  
Qy 481 CTCAGCCTGGCTAGCACAGAGAGAGGAGAAATGGGACCAACCTGAGATATGCGCCT 540  
Db CTCAGCCTGGCTAGCACAGAGAGAGGAGAAATGGGACCAACCTGAGATATGCGCCT 540  
Qy 541 CCTCTGGCTGAGGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGAGTGA 600  
Db CCTCTGGCTGAGGAGAGAAATCTCTGGGTTTCCAGATCTCTGACAGAGAGTGA 600  
Qy 601 TTCTGAGGGCCGCTCTGCTCTGAGACAAATTAAGGGATGAAGTCTGAGAGGATGA 660  
Db TTCTGAGGGCCGCTCTGCTCTGAGACAAATTAAGGGATGAAGTCTGAGAGGATGA 660  
Qy 661 GGGGAAGACAATCCCGGAAGACTGATCAGGGGTTCCCTTGAACCCACAGACGCTTGG 720  
Db GGGGAAGACAATCCCGGAAGACTGATCAGGGGTTCCCTTGAACCCACAGACGCTTGG 720  
Qy 721 CACAGAGACTTTTCCCTCAGGCTTGTCTGTGCTCAGCTCAATGTGTGGGGTGC 780  
Db CACAGAGACTTTTCCCTCAGGCTTGTCTGTGCTCAGCTCAATGTGTGGGGTGC 780  
Qy 781 TGACTCAGCTCTCTGATCCCTTGGCTCCACTCAGTCAAGTCAAGCCGAGGTCCTGCT 840  
Db TGACTCAGCTCTCTGATCCCTTGGCTCCACTCAGTCAAGTCAAGCCGAGGTCCTGCT 840  
Qy 841 CCCCCGCTCAGAGACTAGAACTTTTCCAAAGAAATAGAGATTATCCAGGTGCGCCGTGCC 900  
Db CCCCCGCTCAGAGACTAGAACTTTTCCAAAGAAATAGAGATTATCCAGGTGCGCCGTGCC 900  
Qy 901 AGGCTGCTCTGGGTTCTGTGCTCCCTTCCACCCAGATATCTGTTCAATCTTAAG 960  
Db AGGCTGCTCTGGGTTCTGTGCTCCCTTCCACCCAGATATCTGTTCAATCTTAAG 960  
Qy 961 ATGCTCAGATCCAGGTCGCTGAGTGCATGAGATGCAAGTGCATTAATTTTC 1020  
Db ATGCTCAGATCCAGGTCGCTGAGTGCATGAGATGCAAGTGCATTAATTTTC 1020  
Qy 1021 TGAATCTCTTCAAGACCCCGCAAGACACAGTGAACCCACCTGTCTTGAATAT 1080  
Db TGAATCTCTTCAAGACCCCGCAAGACACAGTGAACCCACCTGTCTTGAATAT 1080  
Qy 1081 GAGGCCACCTGAGGCTCTGGGCTTGTGCTTACCTCGGAGATCATAGACCTGG 1140  
|||||

Db 1081 GAGGCCACCTGAGGCTCTGGGCTTGTGCTTACCTCGGAGATCATAGACCTGG 1140  
Qy 1141 CAGCGGATGGGAGAGACCAGACCCAGAGACCTGAGCTCTGAGACCAAGGCTTCAGAG 1200  
Db CAGCGGATGGGAGAGACCAGACCCAGAGAGCTGAGACTCTGTGAGACCAAGGCTTCAGAG 1200  
Qy 1201 GATGAACTCTCAGAAAGTGGGAGCTGTGTGCTCTTCTGAGAGAGACAGAGATATC 1260  
Db GATGAACTCTCAGAAAGTGGGAGCTGTGTGCTCTTCTGAGAGAGACAGAGATATC 1260  
Qy 1261 ACSTGCCATGTGCAGCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
Db ACSTGCCATGTGCAGCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
Qy 1321 GAGATGAGAGGCAATCAATGCTGTAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
Db GAGATGAGAGGCAATCAATGCTGTAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
Qy 1381 GGTGCTGTGAGAGGCTGGGGTCCAGAGACCTCACCTTCACCTCTTCCAGAGCACT 1440  
Db GGTGCTGTGAGAGGCTGGGGTCCAGAGACCTCACCTTCACCTCTTCCAGAGCACT 1440  
Qy 1441 CTTCCCTGCCACCATCCCATCATGAGGTATGCTGTGCTGAGGAGGAGGAGGAGGAGGAG 1500  
Db CTTCCCTGCCACCATCCCATCATGAGGTATGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Qy 1501 TACTGACTGAGAGCTGGGGTCCGCTGTGCTGTGAGAAAGAGAGACTCAGATGAAGAG 1560  
Db TACTGACTGAGAGCTGGGGTCCGCTGTGCTGTGAGAAAGAGAGACTCAGATGAAGAG 1560  
Qy 1561 GGGTGACAAAGTGGGGTGTGAGTTTCTTGTCCCACTGGGGTTTCAGAGCCCGAGTGAAG 1620  
Db GGGTGACAAAGTGGGGTGTGAGTTTCTTGTCCCACTGGGGTTTCAGAGCCCGAGTGAAG 1620  
Qy 1621 GTGTGCTGCTGCTGTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680  
Db GTGTGCTGCTGCTGTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680  
Qy 1681 CCTGTGTGCGACGACCTTCTCTTTGTAAAGCACTGTGACAAATGAAGAGACAGATTTAT 1740  
Db CCTGTGTGCGACGACCTTCTCTTTGTAAAGCACTGTGACAAATGAAGAGACAGATTTAT 1740  
Qy 1741 TACTTGAATTTGATGATGGGAGCTGATCCCAATCAGAGTCAAGGAGAGAGTGC 1800  
Db TACTTGAATTTGATGATGGGAGCTGATCCCAATCAGAGTCAAGGAGAGAGTGC 1800  
Qy 1801 COTGCTAAGGACAGACCTTGAAGAGGAGTGTGCGAGACCCACATCTGCTTCTTG 1860  
Db COTGCTAAGGACAGACCTTGAAGAGGAGTGTGCGAGACCCACATCTGCTTCTTG 1860  
Qy 1861 TTTTCTGATGCGCCCTGGGTCTGCACTACACATTTCTGGAACCTTCTGAGGCTCAA 1920  
Db TTTTCTGATGCGCCCTGGGTCTGCACTACACATTTCTGGAACCTTCTGAGGCTCAA 1920  
Qy 1921 GACTAGAGGTTCTCTAGAGACCTATGAGCCCTGACACTTCTTGTGCTCTCAGAGACA 1980  
Db GACTAGAGGTTCTCTAGAGACCTATGAGCCCTGACACTTCTTGTGCTCTCAGAGACA 1980  
Qy 1981 TTTTCTCCACAGATTGAAAAGAGAGAGTACTCTCAGGCTGCACTAAGTATGAAG 2040  
Db TTTTCTCCACAGATTGAAAAGAGAGAGTACTCTCAGGCTGCACTAAGTATGAAG 2040  
Qy 2041 AGGCTGATCCCTGAGATCTTGGATCTTGTGGAGAGCCATGAGGAGGAGCTCAGCCAC 2100  
Db AGGCTGATCCCTGAGATCTTGGATCTTGTGGAGAGCCATGAGGAGGAGCTCAGCCAC 2100  
Qy 2101 CCGACAATTCGCTCTGAGACATCTCTGTGCTGTGAGACAGAGTCTGTGTTTGTTC 2160  
Db CCGACAATTCGCTCTGAGACATCTCTGTGCTGTGAGACAGAGTCTGTGTTTGTTC 2160  
Qy 2161 TACTTAAAGCAGTGAAGTGGCCAGGCTCTAATGTCTCTCAGGCTTGTAAATGTGA 2220  
Db TACTTAAAGCAGTGAAGTGGCCAGGCTCTAATGTCTCTCAGGCTTGTAAATGTGA 2220  
|||||



Db 1501 TAGTCACTGGAGCTGCGCTGCTCTGCTGCTGAGAAAGAGCTCAGTAGGAAG 1560  
QY 1561 GGGTACAAAGTGGGGTCTGAGTTTTCTTGTGCCACTGGGGGTTTCAAGCCCCAGTAGAA 1620  
Db 1561 GGGTACAAAGTGGGGTCTGAGTTTTCTTGTGCCACTGGGGGTTTCAAGCCCCAGTAGAA 1620  
QY 1621 GTGTGCCCTGCTGTTACTGTGGGAAGCAACATCCACACTCTATGGGCGCTTACCACCTGGG 1680  
Db 1621 GTGTGCCCTGCTGTTACTGTGGGAAGCAACATCCACACTCTATGGGCGCTTACCACCTGGG 1680  
QY 1681 CCCGTGTGGCAGACCTTCTCTTTTGAAGCACCTGTGCAATGAAGACAGATTTAT 1740  
Db 1681 CCCGTGTGGCAGACCTTCTCTTTTGAAGCACCTGTGCAATGAAGACAGATTTAT 1740  
QY 1741 TACCTTGATGATTTAGTATGGGAGCTGATCCAGTAATCAGAGTCAGAGAGAGTC 1800  
Db 1741 TACCTTGATGATTTAGTATGGGAGCTGATCCAGTAATCAGAGTCAGAGAGAGTC 1800  
QY 1801 CCTGGCTAAGCAGACCTTAGAGAGGAGATTGGTCGAGAGCCACATCTGTTCTCTTG 1860  
Db 1801 CCTGGCTAAGCAGACCTTAGAGAGGAGATTGGTCGAGAGCCACATCTGTTCTCTTG 1860  
QY 1861 TTTTCTCGATGCGCTGGGTCGAGTCACACATTTCTGAAACTTCTCGAGGGTCCAA 1920  
Db 1861 TTTTCTCGATGCGCTGGGTCGAGTCACACATTTCTGAAACTTCTCGAGGGTCCAA 1920  
QY 1921 GACTAGAGAGTTCCTTAGAGACCTTAGGCGCTGCGACCTTCTGGCTCTCACAGACA 1980  
Db 1921 GACTAGAGAGTTCCTTAGAGACCTTAGGCGCTGCGACCTTCTGGCTCTCACAGACA 1980  
QY 1981 TTTTCTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTAATATGAAG 2040  
Db 1981 TTTTCTCCACAGATTTGAAAGAGAGAGTACTCTCAGGCTGCAAGTAATATGAAG 2040  
QY 2041 AGCGTATGATCCCTGAGATCTTGGGATCTTGTGTTGGAGCCATGGGGAGCTCACCCAG 2100  
Db 2041 AGCGTATGATCCCTGAGATCTTGGGATCTTGTGTTGGAGCCATGGGGAGCTCACCCAG 2100  
QY 2101 CCCACAATTCCTCCTGCGCACATCTCCTGCTGCTGCTGACAGAGTCTGTTTTGTTTC 2160  
Db 2101 CCCACAATTCCTCCTGCGCACATCTCCTGCTGCTGCTGACAGAGTCTGTTTTGTTTC 2160  
QY 2161 TACTTAGCAGATGAGATGCCCCAGGCGCTATATGTCTCTCACAGGCTTGTAAATGTGA 2220  
Db 2161 TACTTAGCAGATGAGATGCCCCAGGCGCTATATGTCTCTCACAGGCTTGTAAATGTGA 2220  
QY 2221 CACCCCGGGGGGCTGATGTGTGGGTTGTTAGGGGAACAGGGAGCATAGCTGTGTA 2280  
Db 2221 CACCCCGGGGGGCTGATGTGTGGGTTGTTAGGGGAACAGGGAGCATAGCTGTGTA 2280  
QY 2281 TGAAGTTCTTGTGACTTCAATGTATTGAGCATGTGATGGGCTTTTAAAGTGCACCCCT 2340  
Db 2281 TGAAGTTCTTGTGACTTCAATGTATTGAGCATGTGATGGGCTTTTAAAGTGCACCCCT 2340  
QY 2341 CACTGTGACTGATATGAATTTGTTCAATGAATATTTTCTGTAGTGTAAACAGCTGCCCT 2400  
Db 2341 CACTGTGACTGATATGAATTTGTTCAATGAATATTTTCTGTAGTGTAAACAGCTGCCCT 2400  
QY 2401 GTGTGGAGCTGATGGGCAAG 2420  
Db 2401 GTGTGGAGCTGATGGGCAAG 2420

RESULT 5  
US-09-359-922-598  
; Sequence 598, Application US/09359922  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: 20411-752CON1  
; CURRENT APPLICATION NUMBER: US/09/359, 922  
; CURRENT FILING DATE: 1999-07-22

EARLIER APPLICATION NUMBER: US 09/205,155  
; EARLIER FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 13203  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 598  
; LENGTH: 4465  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-359-922-598

Query Match 72.4%; Score 1768.4; DB 17; Length 4465;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 2126; Conservative 0; Mismatches 281; Indels 59; Gaps 13;

QY 5 CCCGAGTCCCGGGTCCGGATCCACCCCGAGGCCCGGAGCCGCCAGACCTTACCC 64  
Db 1079 CCACAGTCCCGGGTCCGGATCCGAGATCCGCCGAGACCCCGGAGCC--CCGAGACCTTGGCC 1136  
QY 65 TGGAGAAACCCCAAGGGCCCTTACC-----AAAATCCCGC 101  
Db 1137 CGGAGAGAGGCCCAAGGCCCTTTACCCGGTTTCAATTTTCAAGTTTAAAGCCAAAATCCCGCC 1196  
QY 102 GGGTGGTCCGGGCGAGAGGCGAGGCTGGGCGGGGCTGACCGAGGGGCTGGGGCAG 161  
Db 1197 GGGTGGTCCGGGCG-6GGGCGGCTCGGGGAGCGGGGCTGACCGCGGGTCCGGGCGAG 1255  
QY 162 GTTCTCACACCCCTCAGTGTGATTTGGTGCAGCTGGGGTCCGACGAGCCCTCTCC 221  
Db 1256 GTTCTCACACCATCCAGTATATGATTTGATGCTGGCGAGTGGGTCGAGGCGGCTCTCC 1315  
QY 222 CGGGTATGAACAGTATGCTTACGATGGCAAGATTACCTGCGCCCTGAAAGAGAGCTGC 281  
Db 1316 GCGGTACCGGAGAGACCTTACGAGCGCAAGGATTTACATCGCTTACCTTACAGAGAGCTGC 1375  
QY 282 GCTCTGACCGGAGGAGACCTCGGGTCAAGTCTCCAAAGCCGCAAGTGTGAGGCGCCA 341  
Db 1376 GCTCTGACCGGAGGAGACCTCGGGTCAAGTCTCCAAAGCCGCAAGTGTGAGGCGGCC 1435  
QY 342 ATGTGGCTGAACAAAGAGAGAGCTTACCTGAGAGGAGCAGTGGTGGATGCCAGAT 401  
Db 1436 ATGAGCGGAGAGAGTGTGAGAGCTTACCTGATGTGACCTGGTGGAGTGGCTCCGAGAT 1495  
QY 402 ACCCTGAGAGCGGAGAGAGATGCTGCGAGCGGCGGGATCCAGAGGAGCAGTGGGGCTCC 461  
Db 1496 ACCCTGAGAGCGGAGAGAGAGATGCTGCGAGCGGCGGGATCCAGAGGAGCAGTGGGGCTCC 1555  
QY 462 CCTGATCTCTGTAGACCTCTCAGCGCTCAGCAAGAGAGAGAGAAATGGAGCC 521  
Db 1556 CCTGATCTCTGTAGATCTCCCGGGCTGGCTCCCAAGAGGAGAGACAATGGAGACC 1615  
QY 522 AACACTAGATATGCGCCCTCCCTGCTGCTGAGAGAGAGAGAAATCCCTGGGTTCCAG 581  
Db 1616 AACACTAGATATGCGCCCTCCCTGCTGCTGAGAGAGAGAGAAATCCCTGGGTTCCAG 1675  
QY 582 ATTCCTGATCAGAGAGTGTCTGAGGGCCCTCTGCTGCTCTGAGCAATTAAGGAGTG 641  
Db 1676 ATTCCTGATCAGAGAGTGTCTGAGGGCTCTGCTGCTCTGAGCAATTAAGGAGTGA 1735  
QY 642 AAGTCTGAGGAGTGTGAGGAGAGAGACAATCCCTGAGAACTGATCAGGGTTCCTTT 701  
Db 1736 AATCTCTGAGAGAT--GACGGGAAAGACATCCCTGAAATATGATGATGTTCTCCCTTT 1794  
QY 702 GAC--CCACAGCAGCTTGGGACACAGGACTTTTCCCTTCCAGGCTTGTCTGCTCAG 760  
Db 1795 GACACCGGAGAGCTTGGGCGCGTGGAGCTTTTCCCTTCCAGGCTTGTCTGCTCAG 1854  
QY 761 ACTCAATGTGTGGGGTGTGACTGACTCCAGCTCCTGATGCTCCTTGGCTCCACTAGGT 820  
Db 1855 ACTCAATGTGTGGGGTGTGACTGACTCCAGCTCCTGATGCTCCTCAGCTCCACTAGGT 1914  
QY 821 CAGACCGGAGGTCTCTGCTCCCGCTCAGAGACTGAGAACTTTCACAGCAATTAAGAGAT 880  
Db 1915 CAGACCGGAGAGTCTGCTTCCCTC--TTCAGGAGACTGAATTTTCCAGCAATTAAGAGAT 1973

Oy 881 TATCCAGAGTGGCGGTGTCAGAGTGGGTGTCGTCGTCCTTCCACCCAG 940  
 Db 1974 TATCCAGAGTGGCGGTGTCAGAGTGGGTGTCGTCGTCCTTCCACCCAG 2033  
 Oy 941 GTATGATGATCTTATAGATGATGATGATGATGATGATGATGATGATGAT 1000  
 Db 2034 GTATGATGATCTTATAGATGATGATGATGATGATGATGATGATGATGAT 2091  
 Oy 1001 TGCAGAGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060  
 Db 2092 TGCAGAGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2151  
 Oy 1061 ACCACCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1120  
 Db 2152 ACCACCTGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2211  
 Oy 1121 CGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1180  
 Db 2212 CGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271  
 Oy 1181 TGGAGACGAGGCTGTCAGAGGATGAACTTCCAGAGTGGGAGCTGTCCTT 1240  
 Db 2272 TGGAGACGAGGCTGTCAGAGGATGAACTTCCAGAGTGGGAGCTGTCCTT 2331  
 Oy 1241 CTGGAGAGGACGAGATGATGATGATGATGATGATGATGATGATGATGAT 1300  
 Db 2332 CTGGAGAGGACGAGATGATGATGATGATGATGATGATGATGATGATGAT 2391  
 Oy 1301 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360  
 Db 2392 CCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2451  
 Oy 1361 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1420  
 Db 2452 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2491  
 Oy 1421 ACCTGCTTCCAGAGAGTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1480  
 Db 2492 CCTGCTTCCAGAGAGTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2551  
 Oy 1481 CCTGCTTCCAGAGAGTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1540  
 Db 2552 CCTGCTTCCAGAGAGTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2611  
 Oy 1541 GAAAGAGTCAAGTAAAGAGAGAGTGAAGTGGGCTGAGTTTCTTGTCCACTG 1600  
 Db 2612 GAAAGAGTCAAGTAAAGAGAGAGTGAAGTGGGCTGAGTTTCTTGTCCACTG 2671  
 Oy 1601 GTTCAAGAGGAGTAAAGTGAAGTGGGCTGAGTTTCTTGTCCACTG 1660  
 Db 2672 GTTCAAGAGGAGTAAAGTGAAGTGGGCTGAGTTTCTTGTCCACTG 2731  
 Oy 1661 ATGGGCTACCCAGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAG 1720  
 Db 2732 ATGGGCTACCCAGAGTGGGCTGAGTGGGCTGAGTGGGCTGAGTGGGCTGAG 2791  
 Oy 1721 ACAATGAGAGCAATATATATATATATATATATATATATATATATATATAT 1780  
 Db 2792 ACAATGAGAGCAATATATATATATATATATATATATATATATATATATAT 2850  
 Oy 1781 TCACAGGTCAGAGAGTCCCTGTCAGAGAGAGTCCCTGTCAGAGAGAGTCCCTG 1840  
 Db 2851 TCACAGGTCAGAGAGTCCCTGTCAGAGAGAGTCCCTGTCAGAGAGAGTCCCTG 2908  
 Oy 1841 ACCGATATGCTGCTTCTTCTTCTTCTGAT--GCGCTGGGCTGAGTCAACATTTT 1898  
 Db 2909 ACCGATATGCTGCTTCTTCTTCTTCTGAT--GCGCTGGGCTGAGTCAACATTTT 2968  
 Oy 1899 TGGAACTTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1958  
 Db 2969 TGGAACTTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 3028

Oy 1959 CTCTGAGGCTTCACAGAGATTTTCTTCCACAGATTTGAAAGAGGAGCTACTCTC 2018  
 Db 3029 CTCTGAGGCTTCACAGAGATTTTCTTCCACAGATTTGAAAGAGGAGCTACTCTC 3088  
 Oy 2019 AGCTGCAAGTATGATGAGAGGCTGATCCCTGAGATCTTGGATCTTGTGTGGG 2078  
 Db 3089 AGCTGCAAGTATGATGAGAGGCTGATCCCTGAGATCTTGGATCTTGTGTGGG 3148  
 Oy 2079 AG--CCATGAGGAGCTACACCCACCAATTCCTGTCGTCGTCGTCGTCGTCGTC 2137  
 Db 3149 AGCCATGAGGAGCTACACCCACCAATTCCTGTCGTCGTCGTCGTCGTCGTCGTC 3208  
 Oy 2138 CTGACAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2197  
 Db 3209 CTGACAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3268  
 Oy 2198 TCTCTCAGGCTGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2257  
 Db 3269 TCTCTCAGGCTGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 3328  
 Oy 2258 GAACAGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2317  
 Db 3329 GAACAGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3388  
 Oy 2318 GGGCTGTTAAAGTTCACCCCTGATGATGATGATGATGATGATGATGATGATGAT 2375  
 Db 3389 GGGCTGTTAAAGTTCACCCCTGATGATGATGATGATGATGATGATGATGATGAT 3448  
 Oy 2376 TTTCTAGTGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2435  
 Db 3449 TTTCTAGTGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3508  
 Oy 2436 CCTCTT 2441  
 Db 3509 TCCCTT 3514  
 RESULT 6  
 US-09-359-922-598  
 : Sequence 598, Application US/09359922A  
 : GENERAL INFORMATION:  
 : APPLICANT: Leshkowitz, Dena  
 : TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA  
 : FILE REFERENCE: 20411-752CON1  
 : CURRENT FILING DATE: 1999-07-22  
 : EARLIER APPLICATION NUMBER: US 09/205,155  
 : EARLIER FILING DATE: 1998-12-03  
 : EARLIER APPLICATION NUMBER: US 09/034,341  
 : EARLIER FILING DATE: 1998-02-13  
 : NUMBER OF SEQ ID NOS: 13203  
 : SOFTWARE: FastSeq for Windows Version 3.0  
 : SEQ ID NO 598  
 : LENGTH: 4465  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 US-09-359-922-598  
 Query Match 72.4%; Score 1768.4; DB 17; Length 4465;  
 Best Local Similarity 86.2%; Pred. No. 0;  
 Matches 2126; Conservative 0; Mismatches 281; Indels 59; Gaps 13;  
 Oy 5 CCCAGTCTCCGGGTCTGGGATCCACCCGAGGCGCGGGAGCCCGCCAGACCTCTTACC 64  
 Db 1079 CCACAGTCTCCGGGTCTCGAATCCGCCGAAAGCCGCGGGAGCC--CCGAGACCTTGGCC 1136  
 Oy 65 TGGGAGAACCCCAAGGCGCTTACC-----AAATCCCGCC 101  
 Db 1137 CGGAGAGGCGCAGGCGCTTACCCGGTTTCAATTTTCAAGTTTAAAGCCAAATATCCCCC 1196  
 Oy 102 GGGTGGGTCGGGCGAGGCGGAGGCTCGGTGGGCGGGCTGACCGAGGAGGCTGGGCGCAG 161









Db	2612	GAAGAGCTCAGGTGAGAGGGGGTGAAGGGGTGAGGGGTCTGAGATTTCTTGTCCTACCTGAGG	2671
Oy	1601	GTTTTCAAGCCCCAGGTAGAAAGTGTCCCGCTGGTACTGGGAAGCACCATTGCACATCTC	1660
Db	2672	GTTCCAAGCCCCAGCTAGAAATGTCCCGTCTCATTTACTGGAAAGCACTTCCACAATTC	2731
Oy	1661	ATGGGCTACCCAGCTGGGGCCCTGTGTGTCAGACACTTCTCTTTTGTAAAGCACTGTG	1720
Db	2732	ATGGGCGGAGCCAGCTGGGGCCCTGTGTGTCAGACACTTCTCTTTTGTAAAGCACTGTG	2791
Oy	1721	ACATGAAGACAGATTTTATTCCTTGATGATTAAGTATGATGGGAGCTGATCCAGTAA	1780
Db	2792	AAATGAAGACAGATTTTATTCACCTTGATTAAGCGGGTGAT - GGGAGCTGATCCAGCAG	2850
Oy	1781	TCACAGTCCAGGAAGGTGTCCTGGCTAAGACAGACCTTAAAGAGGCACTGGTGAAG	1840
Db	2851	TCACAGTCCACAG - GGAAGGTGTCCTGAGAGCACAACCTCAGAGGGCTATGTGTCAGG	2908
Oy	1841	ACCCACATCTGCTTCTCTGTCTTTTCCAT - GCGCCGTGGGTCCGACATCACATTTT	1898
Db	2909	ACCCACACCTGCTTCTTCAATGTTTCTTATCCCGCCCTGGGTCTGCGATCACATTTT	2968
Oy	1899	TGGAACCTTCCGAGGGTCCACACATAGAGAGTCTCTAGAGCCTCATGCGCTGCGAC	1958
Db	2969	TGGAACTTCTCTGGGGTCCAAACACTAGAGAGTCTCTAGACCTTAAGCGCTGCGCTC	3028
Oy	1959	CTTTCTGGCCTCTCAGACACATTTTCTTCCACAGATTTGAAAGGAGGGAGCTACTCTC	2018
Db	3029	CTTTCTGGTATCTCAGAGCAATTTTCTTCCACAAATGAAAAGAGAGGAGCTACTCTC	3088
Oy	2019	AGGCGCAAGTATATGAAGAGAGGCTGATCCCTGAGATCTTGGGATCTGTGTTGGG	2078
Db	3089	AGGCGCAAGTATATGAAGAGAGGCTGATCCCTGAGATCTTGGGATATGTGTTGGG	3148
Oy	2079	AG - CCATGGGGAGCTCACCCACCACAATTCCTCTCTGGCCACATCTCCTGTGCT	2137
Db	3149	AGCCCATGGGGAGCTCACCCACCACAATTCCTCTCTACCCACATCTCTGTGGAT	3208
Oy	2138	CTGACCAGTCTGTTTTTGTTCACCTGAGGAGTGAAGACAGTGGCCAGGCGCTTAATGTG	2197
Db	3209	CTGACCAGTCTGTTTTTGTTCACCCAGGAGTGAAGATGCCCCAGGGCTCTGATGTG	3268
Oy	2198	TCCTCACAGGCTTGAATATGTGACACCCCGGGGGGCTGATGTGTGGTGTGAGGG	2257
Db	3269	TCTCTACAGCTGTGAAGTGAAGAGCTGTGAGAGGCGCTGATGTGTGGTGGGGCG	3328
Oy	2258	GAACAGGGACATAGCTGTGCTATGAGGTTCTTTGACTTCAATGATATGACATGAT	2317
Db	3329	GAACATGTGACACACTGTGCTATGAGGGGTTCTTTGATGTGATGTGATGACATGCGAT	3388
Oy	2318	GGGCGTAAAGTGTGACCCCTCAGCTGACATGTGAATTTGTTCAATATA - TTT	2379
Db	3389	GGGCGTAAAGTGTGACCCCTCAGCTGACATGTGAATTTGTTCAATATAATTTT	3448
Oy	2376	TTCTAGTGTGAACAGCTGCCCTGTGTGGACTGAGTGGCAAGATTTTGTCATGCTT	2435
Db	3449	TTCTAAGTGTGACAGAGCTGCTGTGTGGAGTGTGAGGCAAGATTTTGTCATGCGCT	3508
Oy	2436	CCCTTT 2441	
Db	3509	TTCCCT 3514	

RESULT 8  
PCT-US02-10055-1722  
SEQUENCE 1722, Application PC/TUS0210055  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Aigate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Gaiger, Alexander  
APPLICANT: Gordon, Brian

```

: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY
: FILE REFERENCE: 210121.572PC
: CURRENT APPLICATION NUMBER: PCT/US02/10055
: CURRENT FILING DATE: 2002-03-19
: NUMBER OF SEQ. ID NOS: 1863
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 1722
: LENGTH: 4000
: TYPE: DNA
: ORGANISM: Homo sapiens
: PCT-US02-10055-1722

Query Match      69.4%; Score 1694.4; DB 1; Length 4000;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 2111; Conservative 0; Mismatches 286; Indels 75; Gaps 17;

```

QY	5	CCGAGTCCTCGGGTCTGGGGATCTCACCCCGAGGCGGGGACCCGCGCAACCCCTTAC	64
Db	1062	CCACAGTCTCCGGGTCCGAGATTCGCCGCCGAGACCCGGGAC--CCGACACCTTGGCC	1119
QY	65	TGGGAGACCCCAAGGCGCCTTAC-----AAAAATCCCGC	101
Db	1120	CGGGAGAGGCCACAGGCGCCTTTACCGGTTTCATTTCAGTTTAGGCCAATAATTCGCC	1179
QY	102	GGGTGGTCCGGGCGAGGCGAGCCTGGTGGGCGGGGCTGACCGAGGGGTGGGGCCAG	161
Db	1180	AGGTTGGTCGGGGGG--GGGGGGGGCTCGGGGGAACGGGCTACCGCGGGTCCGGGCGAG	1238
QY	162	GTTTCACACCCCTTCAGTGGATGATTGGCTGGACCTGGGGTCCGAGGACGCCCTCTCC	221
Db	1239	GTTCTCACACCTCTCAGAGGATGTATGGCTGGGACGTGGGGTCGAGCTGGCGCTCTCC	1298
QY	222	GGGGGTATGAACAGTATGCTTACGATGGCAGAGGATTACTCGCCCTGAAGAGACCTGC	281
Db	1299	GGGGGTATCAACAGTATGCTTACGAGCGGCAAGGATTATCTCCCTGAAGAGACCTGC	1358
QY	282	GGTCTGAGACCGCAGCGGACACTGCGGGCTCAGTCTCCAGGGCAGAGTGTAGCGGCCA	341
Db	1359	GGCTGTGAGACCGCGCGGACATGGCAGCTTACAGCACAGACAGAGTGGGAGGGGCC	1418
QY	342	ATGTGGCTGAACAAAGAGAGACCTACCTGGAGGGCACGTGCTGGATGGCTCCACAGAT	401
Db	1419	ATGTGGCGGAGAGATTGAGAGACCTACCTGGAGGGCACGTGGAATGGCTCCGCGAGAT	1478
QY	402	ACCTGAGACGGGAGAGAGATGCTGAGCGCGCGGGTACAGGGGGCAGTGGGGGCGCTC	461
Db	1479	ACCTGAGACGGGAGAGAGAGCTGTGAGGGCACGGGTACAGGGGGCCACGSGGGGCTC	1538
QY	462	CCGATCTCTGTACACTCTCAGCCTCGGGCTAGCACAGAGAGAGAGAAATATGGGAC	521
Db	1539	CCGATCTGCGCTTAAATCTCCCGGGCTGGGCTCCACAGAGAGGGGAGACAAATTGGGAC	1598
QY	522	AACACTGAAATATCGCCCTCCCTCTGGTCTGAGGAGAGAAATCTCTGGGTTTCAG	581
Db	1599	AACACTGAAATATCGCCCTCCCTCTGGTCTGAGGAGAGAGAAATCTCTGGGTTTCAG	1658
QY	582	ATCCTGTACCAAGAGTATTTCTAGAGCGCCGCTCTGCTCTCGGGACAAATTAAGGATG	641
Db	1659	ATCCTGTACCAAGAGTATTTCTAGAGTTCGGGCTCTGCTCTGACACAAATTAAGGATA	1718
QY	642	AAGTCCTGAGGAGTGGAGGAGGAGAAACAATCCCTGGAGAGACTGATCAGGGGTTCC	701
Db	1719	AAATCTCTGAGGAAT--GACGGGAAGAGATCCCTGSAATAGATGATGGTTCCCTTT	1777
QY	702	GAC-----CCACAGCAGGCTTGGGACCAAGACTTTTCCCTTAGGCCTTTGTCTCTGC	756
Db	1778	GACACACAGCAGGAGCAGGCTTGGGCGCGGACCTTTCCTCTAGGCGCTTGTCTCTCT	1837
QY	757	TGCACACTCATGTGCTGGGGGCTGATCCAGTCTCTGAGTCCCTTGGCGCTCACATC	816
Db	1838	TGCACACTCATGTGCTGGGGGCTGAGTCTCAGATCCACGACTTCTGATGCTTACGCTCAC	1897

QY	817	AGGTCAGAACCGGAGGAGGTCCTGGCTGCCCCGCTCAGAGACATGAAACCTTCCAGGAAATATGG	876
Dp	1898	AGGTCAGAACCGGAGGAGGTCCTGGCTGCCCCGCTCAGAGACATGAAACCTTCCAGGAAATATGG	1955
QY	877	AGATTATCCAGAGTGCCCGTGCCAGGCGTGGTGTGGGTTCTGTGCTCCCTTCCCTCACCC	936
Dp	1956	AGATTATATCCAGAGTGCCCGTGCCAGGCGTGGTGTGGGTTCTGTGCTCCCTTCCCTCACATC	2015
QY	937	CCAGGATATCGGTCATTCTTTAGAGATGTACATCCAGAGTGCGTGCGAGGTGTCCCATGA	996
Dp	2016	CCAGGATGTCGTGTCCATTCTTCAGATGCCACAT--GTGTGCTGGAGAGGTGTCCCATGA	2073
QY	997	GAGATGCCAAGTGCTTGAATTTTCTGACTCTTCCCTTTCAGACCCCCCAAGACACACGTG	1056
Dp	2074	CAGATGCCAATAATGTCTGAATGATCTGCTCTTCACAGACGCCCCCCAAGACGATATYG	2133
QY	1057	ACCACCAACCCCTGCTTTTGACTATGAGAGCCACCTGAGGTGCGGGGCCCTCGGGCTTTTAC	1116
Dp	2134	ACTCACCAACCGTGCTCTGTACACATGAAAGCACCTTATAGGTGCTGGGGCCTTGAGCTTTTAC	2195
QY	1117	CTCGCGAGATCATATCTGACCTGGCAGCGGGATGSGGAGAGCACAGCCAGGACGTGGAG	1176
Dp	2194	CTCGCGAGATCATACACTGACCTGGCAGCGGGATGSGGAGAGCACAGCCAGGACACGAGAG	2255
QY	1177	CTCGTGAGAGACAGGCGCTGAGAGGGATGGAACCTTCCAGAAATGGGACACTGTGGTGGG	1236
Dp	2254	CTCGTGAGAGACAGGCGCTGAGAGGGATGGAACCTTCCAGAAATGGGACGCTGTGGTGGG	2313
QY	1237	CCTTCTGGAAGAGACAGAGATACACGTGCCATGTGCACATGAGAGGGCTGCCGAGCC	1296
Dp	2314	CCTTCTGGAAGAGAGAGAGATACACCTGTGCCATGTGCACATGAGAGGGTGTGCCAAGCC	2375
QY	1297	CTCATGTGAGATGAGATTAAGAGAGGAGATGAGAGCATATGCTCTTTTGGGAAAGACAG	1356
Dp	2374	CTCATCCGTGAGATGAGGATTAAGAGAGGAGAGAGGGGGTGTATGCTTTTGGGAAAGACAG	2433
QY	1337	AGCCTCTCTGAAGACCTTTTAACAGGGTCGGTGTAGAGGCTGGGGGTACAGAACCTTCAC	1418
Dp	2434	AGCCTCTCT--GACCTTTTAGA-----GGGTAGAGGCCCTCTTAC	2470
QY	1417	CTTCCACCTCCTTTCCAGAGACAGCTCTCCCTGGCCACCATCCCATCATGAGGGTATGCTTG	1478
Dp	2471	CTTCCCTCCTTTTCCAGAGACCGCTCTTCCAGCCACCATCCCATCATGAGGGTATGCTTG	2533
QY	1477	CTGGCCTGCTGTCTCTTGACAGCTGTATCTACTGTGAGCTGCGGTGCTGTGTGTGGA	1536
Dp	2531	CTGGCCTGCTGTCTCTTGAGAGCTGTATCTACTGTGAGCTGTGCTGTGTGTGGA	2590
QY	1537	GAAAGAAAGAGCTCAGGTAAAGAAAGGGGTGCAAGTGGGTCTGTAGTTTCTGTGCCACT	1596
Dp	2591	GGAGGAAAGAGCTCAGGTGGGGGAAAGGGGTGA--AAGGTGGGTGTGAAGTTCTTGTCTACT	2644
QY	1597	GGGGGTTTCAAGGCCCCAGGTAAAGAAAGTGTGCGCTGCTGTACTGTGGAAGACCATCCAC	1656
Dp	2650	GAGGGTTTCAAGAGCCAGGTAAAGAAAGTGTGCGCTGCTGTACTGTGGAAGACCATCCAC	2705
QY	1657	ACTCATGGGCTTACCGAGCTGGGGCCTGTGTCCAGACACTTCTCTTTTGTAAAGACAC	1718
Dp	2710	AATTATGGGCTTACCGAGCTGGGGCCTGTGTCCAGCACTTACTCTTTTGTAAAGACAC	2765
QY	1717	TGTGACATGAAGACAGATTTATTTACTTGTGATGTGATGATGATGAGGAGACTGATCCCA	1778
Dp	2770	TGTTAAATGAAGACAGATTTATTTACTCTGTGATTTAAGCGGTGAT--GGAGCTGTATCCCA	2828
QY	1777	GTAATCAACAGT--CAGGAAAGAGTCCCTGGGCTTAAGACAGACACTTAAAGAGGAGGAGTTGG	1834
Dp	2829	GCAGTCACAACTCAGCGGGAAGAGTCCCT-----GAGAGACTTCAAGAGGGCGGTTGG	2881
QY	1835	TTCGAGAGCCACATCTGCTTCTCTGTGTTTTCTGAT--CGCCCTGAGGTCTCACTACACA	1895
Dp	2882	TTCAGAGAGCCACATCTGCTTCTCTGATGTTTTCTCTGTATCCGCGCTGTGAGGTCTCACTACACA	2941

Oy	1893	CATTTCGSAACATCTCCMGAGGTCCACAGACTAGAGAGGTCTCCTTAGSACCCTAATGGCCC	1952
Dd	2942	CATTTCGGAATACTTCTCTAGAGTCCCAAGACTGSGAGSTTCTCTAGSACCTTAABGCC	3001
Oy	1953	TGCACCTTTCTTGCGCCTGTCCACAGCATATTTCTTCCACAGATTGAANAAGSGAGCT	2012
Dd	3002	TGACTCTTTTTCTTGATGTATCTCACAGGACATTTCTTCCACAGATTGAANAAGSGAGGCT	3061
Oy	2013	ACTCTCAGGCTGCACACTAAAGTATGAAGAAGGCTGATCCCTAGATCCCTTGGATCTTTGTG	2072
Dd	3062	ACTCTCAGGCTGCACAGTAAGTATGAAGAAGGCTGATCCCTAGATCCCTTGGATATTGTG	3121
Oy	2073	TTTGGGAG--CCATGGGGGAGCTCACCACCCACCAATTTCTCTCTTGCCCCATCTTCG	2131
Dd	3122	TTTGGGAGCCCAATGGGAGGCTCACCCACCCACCAATTTCTCTCTTGCCCCATCTTCG	3181
Oy	2132	TGATCTCTGCACAGGCTGCTTTTTTGTCTCTACTCTAGGACAGTGCACATGGCCAGGCTCT	2191
Dd	3182	TGGATCTGCACAGGCTGCTTTTTTGTCTCTACTCTAGGACAGTGCACATGGCCAGGCTCT	3241
Oy	2192	AATGTCTCTCAGGCTGCTTGAATGTAGACACCCCGGGGGGCTGATGTGTGGTGTGT	2251
Dd	3242	GATGTCTCTCAGGCTGCTTGAATGTAGACACCCCGGGGGGCTGATGTGTGGTGTGT	3301
Oy	2252	TGAGGGGAACAAGGGGACATAGCTGTGCTATAGAGATTTCTTGACTTCATATGTATGAGA	2311
Dd	3302	TGGGGGAACAAGGGGACACAGCTGTGCTATAGAGATTTCTTGACTTCATATGTATGAGA	3361
Oy	2312	TGTATGGGCTGTTTAAAGTACACCCCTCAGCTGTAGATGATTAAGATTGTTCATGANT	2371
Dd	3362	TGGATGGGCTGTTTAAAGTACACCCCTCAGCTGTAGATGATTAAGATTGTTCATGANT	3421
Oy	2372	A--TTTTCGTAGCTGTAAACAGCTGCCCTGTGTGGGACTGAGTGCACATTTGTCTCA	2429
Dd	3422	ATTTTTCGTATAGTGTGTAGACAGCTGCCCTGTGTGGGACTGAGTGCACATTTGTCTCC	3481
Oy	2430	TGCCTTCCTTT 2441	
Dd	3482	TGCCCTTCCTTT 3493	
 RESULT 9 US-10-102-524-1722 ; Sequence 1722, Application US/10102524 ; GENERAL INFORMATION: : APPLICANT: Algate, Paul A. : APPLICANT: Mannion, Jane : APPLICANT: Gaiger, Alexander : APPLICANT: Gordon, Brian : APPLICANT: Harlocker, Susan L. : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE : FILE REFERENCE: 210121.572 : CURRENT APPLICATION NUMBER: US/10/102,524 : NUMBER OF SEQ ID NOS: 1863 : SOFTWARE: FastSeq for Windows Version 4.0 : SEQ ID NO 1722 : LENGTH: 4000 : TYPE: DNA : ORGANISM: Homo sapiens US-10-102-524-1722			
 Query Match                 69.4%; Score 1694.4; DB 40; Length 4000; Best Local Similarity      85.4%; Pred. No. 0; Matches 2111; Conservative 0; Mismatches 286; Indels 75; Gaps 17;			
Oy	5	CCGAGTCTCGGGGTCTGGGATCCACCCCGAGGCGCGGAGCCCGCCAGACCTCTACC	64
Dd	1062	CCACAGTCTCGGGGTCTCGGATCCCGCCCGAGACCGCGGAGC--CCGAGACCTTGGCC	1119
Oy	65	TGGGAGAACCCAGGCGGCTTTACC-----AAAAATCCCGC	101

Db 1120 CCGAGAGAGGCCAGGGCCCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAAATCCCCC 1179  
Qy 102 GGGTGGGTCGCGGAGGAGGAGCTCGGTGGGCGGGGCTGACCGAGGGGGTGGGCCAG 161  
Db 1180 AGGTTGGTGGGGGCG-GGGGGGGGCTCGGGGGAGCCGGCTGACCCGGGGTTCGGGGCCAG 1238  
Qy 162 GTTCTCAGACCCCTCAGTGGATGTTGGCTGGACCTGGGGTTCGACGAGACCTCTCC 221  
Db 1239 GTTCTCAGACCCCTCAGTGGATGTTGGCTGGACCTGGGGTTCGACGAGACCTCTCC 1298  
Qy 222 GCGGATGAAACAGTATGCTTAGATGGCAAGGATTACGCGCCCTGAACGAGAGACTCC 281  
Db 1299 GCGGATGAAACAGTATGCTTAGATGGCAAGGATTACGCGCCCTGAACGAGAGACTCC 1358  
Qy 282 GCTCCCTGACCGGAGCGACATCGCGCTCAGATCTCCACAGCGCAAGTGTAGCGCGCCA 341  
Db 1359 GCTCTTGAGCCGGCGGAGATGGCAGCTCAGACCAACAGCAAGTGTAGCGCGGCC 1418  
Qy 342 ATGTGGCTGAACAAAGAGAGCTACCTGAGAGGCGACGTGGGTGGGTGGCTCCACAGAT 401  
Db 1419 ATGTGGCGGAGCACTTAGAGCCCTACCTGGAGGGGACGTGGGTGGGTGGGTGGGT 1478  
Qy 402 ACCTGGAGAACGGGAGAGAGATGCTGACGCGCGGGGTACACAGGCGAGTGGGGCGCTC 461  
Db 1479 ACCTGGAGAACGGGAGAGAGATGCTGACGCGCGGGGTACACAGGCGAGTGGGGCGCTC 1538  
Qy 462 CCTGATCTCTGTAGACCTCTCAGCCTGAGCTGACACAGAGAGAGAGAAATGGGACC 521  
Db 1539 CCTGATCTCTGTAGACCTCTCAGCCTGAGCTGACACAGAGAGAGAGAAATGGGACC 1598  
Qy 522 AACACTGAATATGCGCCCTCCCTGCTGCTGAGGAGAGAGAAATCCCTGGGTTCACG 581  
Db 1599 AACACTGAATATGCGCCCTCCCTGCTGCTGAGGAGAGAGAAATCCCTGGGTTCACG 1658  
Qy 582 ATCTGCTACAGAGAGATGATCTGAGGGGCCCTGCTGCTGAGCAATTAAGGAGT 641  
Db 1659 ATCTGCTACAGAGAGATGATCTGAGGGGCCCTGCTGCTGAGCAATTAAGGAGT 1718  
Qy 642 AAGTCTGAGGAGTGGAGGGGAAAGACATCCCTGGAAGACTGATAGGGGTTCCCTT 701  
Db 1719 AAGTCTGAGGAGTGGAGGGGAAAGACATCCCTGGAAGACTGATAGGGGTTCCCTT 1777  
Qy 702 GAC-----CCACAGCAGCCTTGGACAGAGACTTTTCCCTCGGCCCTTGTCTGCC 756  
Db 1778 GACACACAGGAGCAGCAGCTTGGGCCGCTGACCTTTCTCTCAGGCCCTTGTCTGCC 1837  
Qy 757 TCACACTCAATGTGTGTGGGGTCTGACTCAGCTCCTGAGTCCCTGGGCTCCACTC 816  
Db 1838 TCACACTCAATGTGTGTGGGGTCTGACTCAGCTCCTGAGTCTTCAAGCTCCACTC 1897  
Qy 817 AAGTCAAGAACGGAGTCCCTGCTCCCGGCTCAGAGACTGAACCTTCCAAAGAAATAG 876  
Db 1898 AAGTCAAGAACGGAGTCCCTGCTCCCGGCTCAGAGACTGAACCTTCCAAAGAAATAG 1955  
Qy 877 AGATTATCCAGAGTCCCGCTGCTCAGGCTGTGTCTGGGTTCTGTGCTCCCTGCCACC 936  
Db 1956 AGATTATCCAGAGTCCCGCTGCTCAGGCTGTGTCTGGGTTCTGTGCTCCCTGCCACC 2015  
Qy 937 CCAGGATGTGTTCTATTTAGAGTGTGCACATCCAGAGTCTGCTGAGAGTCCCATGA 996  
Db 2016 CCAGGATGTGTTCTATTTAGAGTGTGCACATCCAGAGTCTGCTGAGAGTCCCATGA 2073  
Qy 997 GAGATGCAAGAGTGTGATTTTCTGACTCTCTTTCAGACCCCGCCCAAGACACTGTG 1056  
Db 2074 GAGATGCAAGAGTGTGATTTTCTGACTCTCTTTCAGACCCCGCCCAAGACACTGTG 2133  
Qy 1057 ACCACACACCTGTCTTTGACTATGAGGCCACCTGAGTGTGGGCTTGGGCTTCTAC 1116  
Db 2134 ACACACACCTGTCTCTGACCATGAAGCCACCTGAGGTGTGGGCTTGGGCTTCTAC 2193  
Qy 1117 CTTGGGAGATCTACTGACCTGGCAGGGGAGAGAGAGACACAGACAGAGAGTGTAG 1176  
Db 2194 CTTGGGAGATCTACTGACCTGGCAGGGGAGAGAGAGACACAGACAGAGAGTGTAG 2253  
Qy 1177 CTGCTGAGAACACAGGCTCGAGGGGATGGAACCTTCCAGAGTGGGACGTGTGTGTG 1236  
Db 2254 CTGCTGAGAACACAGGCTCGAGGGGATGGAACCTTCCAGAGTGGGACGTGTGTGTG 2313  
Qy 1237 CTTCTGAGAGAGAGAGATACAGTGCATGTGACAGCATGAGGGGCTGCCGAGCC 1296  
Db 2314 CTTCTGAGAGAGAGAGATACAGTGCATGTGACAGCATGAGGGGCTGCCGAGCC 2373  
Qy 1297 CTCATGCTGAGATGAGATGAAGAGAGATGAGAGCATATGTCTGTATGGAAGAGAG 1356  
Db 2374 CTCATGCTGAGATGAGATGAAGAGAGATGAGAGCATATGTCTGTATGGAAGAGAG 2433  
Qy 1357 AGCCTCTGAAAGACCTTTTAAAGGGGTGCTGTAGAGGCTGGGGTCCAGAGACCTCAG 1416  
Db 2434 AGCCTCTGAAAGACCTTTTAAAGGGGTGCTGTAGAGGCTGGGGTCCAGAGACCTCAG 2470  
Qy 1417 CTTCACCTCTCTTCCAGAGCAGTCTTCCCTGACCATATCCCATATGATATCTTTG 1476  
Db 2471 CTTCACCTCTCTTCCAGAGCAGTCTTCCCTGACCATATCCCATATGATATCTTTG 2530  
Qy 1477 CTGGCTGTGTGCTCTTGTGAGCTGTACTGACCTGGGCTGGGCTGGGCTGGGCTGGA 1536  
Db 2531 CTGGCTGTGTGCTCTTGTGAGCTGTACTGACCTGGGCTGGGCTGGGCTGGGCTGGA 2590  
Qy 1537 GAAAGAGAGCTCAGATTAAGAGGGGTGACAAGTGGGCTGTAGTGTCTTGTCCACT 1596  
Db 2591 GAAAGAGAGCTCAGATTAAGAGGGGTGACAAGTGGGCTGTAGTGTCTTGTCCACT 2649  
Qy 1597 GGGGCTTCAAGCCCGAGATGAAGTGTGCTGCTGCTGCTTACTGGGAGACCATATCC 1656  
Db 2650 GGGGCTTCAAGCCCGAGATGAAGTGTGCTGCTGCTGCTTACTGGGAGACCATATCC 2709  
Qy 1657 ACTCATGGGCTTCAAGCCCGAGATGAAGTGTGCTGCTGCTTACTGGGAGACCATATCC 1716  
Db 2710 ACTCATGGGCTTCAAGCCCGAGATGAAGTGTGCTGCTGCTTACTGGGAGACCATATCC 2769  
Qy 1717 TGTGCAATGAAGACAGATTTTATCTGATGATGATGATGATGATGATGATGATGATGAT 1776  
Db 2770 TGTGCAATGAAGACAGATTTTATCTGATGATGATGATGATGATGATGATGATGATGAT 2828  
Qy 1777 GTATTCACAGT--CAGAGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1834  
Db 2829 GTATTCACAGT--CAGAGAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2881  
Qy 1835 TCGAGAGCCACATCTGCTTCTGTTCTGTTCTGAT--CGCCCTGGGCTGAGCTACA 1892  
Db 2882 TCGAGAGCCACATCTGCTTCTGTTCTGTTCTGAT--CGCCCTGGGCTGAGCTACA 2941  
Qy 1893 CATTTCTGAAACCTTCTCGAGGCTCAGAGCTAGAGGTTCTCTAGGACTCATGGGCC 1952  
Db 2942 CATTTCTGAAACCTTCTCGAGGCTCAGAGCTAGAGGTTCTCTAGGACTCATGGGCC 3001  
Qy 1953 TGCACCTTGTGGGCTCTCAGAGACATTTTCTCCACAGATTTGAAAGAGAGGAGCT 2012  
Db 3002 TGCACCTTGTGTGTATCTCAGAGACATTTTCTCCACAGATTTGAAAGAGAGGAGCT 3061  
Qy 2013 ACTCTCAGGCTGCAAGTATGATGAAGAGGCTGATCCCTGATATCTTGGGATCTGTG 2072  
Db 3062 ACTCTCAGGCTGCAAGTATGATGAAGAGGCTGATCCCTGATATCTTGGGATTTGTG 3121  
Qy 2073 TTTGGGAG--CGATGGGGGAGTCAACCCCGCAATTCCTCTGAGCAGATCTTCTG 2131  
Db 3122 TTTGGGAGCCAGTGGGGAGTCAACCCCGCAATTCCTCTGAGCAGATCTTCTG 3181  
Qy 2132 TGGTCTGACAGAGTGTGTTTGTGTTTGTCTACTAGGAGTGAAGTGTGAGGCTCT 2191  
Db 3182 TGGGATCTGACAGGTTCTGTTTGTGTTTGTCTACTAGGAGTGAAGTGTGAGGCTCT 3241  
Qy 2192 AATGTGTCTCTCAGGCTTGTATATGTGACACCCCGGGGGGCTGTATGTGTGGTGT 2251  
Db 3242 GATGTGTCTCTCAGGCTTGTATATGTGAGGCTGTGAGGCTGTATGTGTGGTGT 3301

[illegible]

```

RESULT 10
US-09-881-797-3590
: Sequence 3590, Application US/09881797
:
: GENERAL INFORMATION:
:
: APPLICANT: TIM KATH
:
: TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
: RELATING TO RESPIRATORY DISEASES AND OBESITY
:
: FILE REFERENCE: HMO1-04
:
: CURRENT APPLICATION NUMBER: US/09/881,797
:
: PRIOR FILING DATE: 2001-06-14
:
: PRIOR FILING DATE: 2000-06-14
:
: NUMBER OF SEQ ID NOS: 4687
:
: SOFTWARE: FASTSEQ for Windows Version 4.0
:
: SEQ ID NO 3590
:
: LENGTH: 5030
:
: TYPE: DNA
:
: ORGANISM: Human
US-09-881-797-3590

```

Query Match	67.5%;	Score 1648.2;	DB 33;	Length 5030;
Best Local Similarity	84.7%;	Pred. No. 0;		
Matches 2107; Conservative	0;	Mismatches 303;	Indels 77;	Gaps 20;

QY	448	CAGTGGGCGGCTCCCGGATCTCTGTGAACCTCTAGCCCTGG - CCTAGACAAAGAG	506
Db	2243	CGAGGGGCGCTCCCGATGCGCTGTGATATTCGCCGGGCTGGCCCTCCCAAGAGAGG	2302
QY	507	GAGGAATAATGGGACCACTAGATATATGCCCTCCCTCTGGTCTGAGGAGAGAAATC	566
Db	2303	GAGACAAATTTGGGACCAACACATGAAATATGCCCTCCCTCTGGTCTTGAAGGAGAGAAATC	2362
QY	567	CTCCGCGGGTTTTCCAGATTCGTGACCGAGAGTGATTTCTAGGGGCCGTCCTGCTCGG	626
Db	2363	CTCCGCGGGTTTTCCAGATTCGTGACCGAGAGTGATTTCTAGGGTTCCGCCCTCTCTCTGA	2422
QY	627	GACAAATTAAGSAGATGAATCTGTGAGGAGATGGAGGGAAGCAATCCCTGGAGACTGA	686
Db	2423	CACAAATTAAGSAGATGAATATCTGTGAGGAGAT - GAGGGAAGAGCAATCCCTGGAAATCTGA	2481
QY	687	TCAGGCGTCCCTTTGAG - ----CCACAGCACCTTTGGCACAGACTTTTCCCTCTAG	741
Db	2482	TGACTGGTTCCCTTTGACACACACCGGACACACCTTTGGGCCCTTGACTTTTCTCTCTAG	2541
QY	742	GCCTTGTCTCTGCGCTCAGAC - TCAATGTGTGTGGGGGTCTGACTCCAGCTCTCTGAGT	800
Db	2542	GCCTTGTCTCTGTCTTAAACTTAAATGTGTGGGGGTCTGACTCCAGCACTCTCTGAGT	2601
QY	801	CCCTTGGCCCTCACTCGAGTCCAGACCGGAGGTCCTGCTCCCGCTCAGAGACTTAA	860
Db	2602	CCCTCAGCCTCCACTCAGGTCCAGGACCGAGACCAAGTCTGTTCCCTC - TTCAGGGACTTAA	2660
QY	861	CTTTCAAGGAATGAGGAATTAATCCAGGTGCCGTCTCAGGCTGTGTGTGGTTCTG	920
Db	2661	TTTTTCCACGGAAATGGAGATTAATCCAGGTCGCTGTCTCAGGCTGTGTGTGGTTCTG	2720
QY	921	TGCTCCCTTTCCCAACCCCAAGTATTCGGTTCATCTTTAGAGTGACACATCCAGTCTG	980
Db	2721	TGCTCCCTTTCCCAATCCCAAGTGTCTCTGTCTCAATTCAGAGATAGCCAAAT - GTGTCTG	2778
QY	981	CTGAGATGTCCCATGAGAGATGCAAAATGCTTGAATTTTCTGACTCTCTTTAGACC	1040
Db	2779	GAGGAGTGTCCCATGAGAGATGCAAAATGCTTGAATTTTCTGACTCTCTTCCAGACGC	2838
QY	1041	CCCCAAGACACACTGTGACCCACACACCTGTCTTTGACTATGAGGCCACCTCAGTCTG	1100
Db	2839	CCCCAAGACGATGTGACTCACCCAGCTGTCTGTCTGACATGAGGCCACCTCAGTCTG	2898
QY	1101	GGCCCTGGGCTTCTACCTCTGCGAGATCATCTGACTCTGGCAGCCGGATGGGAGAGACA	1160
Db	2899	GGCCCTGAGCTTCTACCTCTGCGAGATCATCACTGACTCTGGCAGCCGGATGGGAGAGACA	2958
QY	1161	GACCCAGAGACTGTGAGCTCTGTGAGACACAGGCTGTGAGGGATGTGAACTTCCAAAGTG	1220
Db	2959	GACCCAGAGACAGGAGCTGTGTGAGAGACAGGCTGTGAGGGATGTGAACTTCCAAAGTG	3018
QY	1221	GGCAGCTGTGTGTGCTGCTTCTGTGAGAGAGAGAGAAATACACTGTGCTATGTGCACATGA	1280
Db	3019	GCGCTGTGTGTGTGCTTCTGTGTGAGAGAGAGAGAAATACACTGTGCTATGTGCACATGA	3078
QY	1281	GGGGCTGGCCGAGGCCCTCATGTGTGAGATGGAATTAAGGAGGGAGATGAGAGCATATCTC	1340
Db	3079	GGGCTGTGGCCAGGCCCTCATGCCCTGAGATGGGTAAAGGAGGAGAGCGGGGCTGATCTC	3138
QY	1341	TGTTAAGGAAMGAGGAGGCTCTCTGAAGACTTTTAACAGGGTGGTGTGTGAGGGCTGG	1400
Db	3139	TTTTAAGGAAMGAGGAGGCTCTCTGAGACTTTTGA - -----G	3178
QY	1401	GATCAGAGACCCCTACCTCACTCTCTTTCCAGAGACACTCTTTCCCTGCCACATCCC	1460
Db	3179	GATCAGAGGCCCTCCTCACTCTCCCTCTTTTCCAGAGACCAATCTTCCAGGCCACCGTCCC	3238
QY	1461	ATCAGTGGTATACGTTGTGTGGCGGTGTTTCCTTTGACGTATGATCATGTAGTCAAGTCCGCTC	1520
Db	3239	ATCAGTGGGCAATCTGTGTGGCGGTGTTTCCTTTGAGGCTGTGATCATGTAGTCAAGTCCGCTC	3298
QY	1521	GCTGCTGTGCTGTGAGAAAGAGACTCAGTTAAGGAAGGGGTGACAAATGGGGTCTGA	1580

```

Db 3299 GCTGCTGATGATGGAGAGAACAGCTAGTGGAGAGGGGTGAGGGGGGTCTGA 3358
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1581 GTTTCCTTGTCCACTGGGGGTTTCAGCCCCAGTAGAGTGTGCCCTGCTGTTACT 1640
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3359 GATTCTGTCTCAGAGAGGTTCCAAAGCCAGCTAAAGATGTCCTGCTCATTA 3418
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1641 GGGAGAGCATCATCAGATGAGGCTTACCCAGCTGGGCGCTGTGGAGACCTTC 1700
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3419 GGGAGAGCATCATCAGATGAGGCTTACCCAGCTGGGCGCTGTGGAGACCTTC 3478
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1701 TCTTTTGAAGACCTGTGTGACATGAGAGACATGATTATTAATCTGTGATGTTAGTGA 1760
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3479 TCTTTTGAAGACCTGTGTGACATGAGAGACATGATTATTAATCTGTGATGTTAGTGA 3538
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1761 TGGGAGACCTGATCCAGTATATCAGAGTACAGAGAGAGTCCCTGGCTAAGAGACCTT 1820
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3539 T-GGGACCTGATCCAGTATATCAGAGTACAGAGAGAGTCCCTGGCTAAGAGACCTT 3595
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1821 AGGAGGCACTGTGTGAGAGACCATCTGCTTCTCTTGTCTGTATC--GCCCTG 1878
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3596 TGGAGGGCGATGTGTCCAGGGGCCACATCTGCTTCTCATGTCTCATCTGACCTG 3655
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1879 GGTCTGAGTACACATTTCTGGAACCTCTGAGGGTCCAAAGCTAGAGGTTCTCTTA 1938
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3656 GGTCTGAGTACACATTTCTGGAACCTCTCTGAGGGTCCAAAGCTAGAGGTTCTCTTA 3715
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1939 GGAACCTCAGTCCCTGACAC--CTTCTGTGCTCTCAGAGACATTTCTTCCACAGATT 1997
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3716 GGAACCTCAGTCCCTGACAC--CTTCTGTGCTCTCAGAGACATTTCTTCCACAGATA 3775
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1998 GAAAGAGGAGGACCTCTCAGGCTGCAAGTATGAGAGAGGCTGATCCCTGAGAT 2057
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3776 GAAAGAGGAGGACCTCTCAGGCTGCAAGTATGAGAGAGGCTGATCCCTGAGAT 3835
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2058 CTTTGGATCTGTGTTGGAG--CCATGGGGAGCTGACCCCAACCAATTCCTCTC 2116
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3836 CTTTGGATCTGTGTTGGAG--CCATGGGGAGCTGACCCCAACCAATTCCTCTC 3895
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2117 TGGGCAATCTCTGTGTCTCTGACAGGCTGCTGTTTGTCTTACTCTGAGAGTAC 2176
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3896 TGGGCAATCTCTGTGTCTCTGACAGGCTGCTGTTTGTCTTACTCTGAGAGTAC 3955
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2177 AGTGCCAGGCTCTATGTCTCTCAGGCTTGAATGTGACACCCCGGGGGGCTG 2236
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3956 AGTGCCAGGCTCTATGTCTCTCAGGCTTGAATGTGACACCCCGGGGGGCTG 4015
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2237 ATGTGTGTGGTGTGAGGGGAAAGGAGATACCTGTCTATGAGGTTCTTGTACT 2296
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4016 ATGTGTGTGGTGTGAGGGGAAAGGAGATACCTGTCTATGAGGTTCTTGTACT 4075
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2297 TCAATGTATGAGATGTGAGGCTTAAAGTGTACCCCTCAGCTGACTGATATG 2356
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4076 TGAATGTATGAGATGTGAGGCTTAAAGTGTGTGACCCCTCAGCTGACTGATATG 4135
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2357 AATTGTCTCAAGTA--TTTTCTGTAGTGAAGACACTCCCTGTGTGGAGTGA 2414
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4136 AATTGTCTCAAGTA--TTTTCTGTAGTGAAGACACTCCCTGTGTGGAGTGA 4195
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2415 GGCAGATTGTTCATGCTTCCCTT 2441
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4196 GGCAGATTGTTCATGCTTCCCTT 4222
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 11  
US-10-021-698-3590, Application US/10021698

; Sequence 3590, Application US/10021698  
; GENERAL INFORMATION:  
; APPLICANT: Tim Keith  
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY  
; FILE REFERENCE: HMO01-04  
; CURRENT APPLICATION NUMBER: US/10/021,698

CURRENT FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: 60/211,749  
PRIOR FILING DATE: 2000-06-14  
NUMBER OF SEQ ID NOS: 4687  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3590  
LENGTH: 5030  
TYPE: DNA  
ORGANISM: Human  
US-10-021-698-3590

Query Match 67.5%; Score 1648.2; DB 38; Length 5030;  
Best Local Similarity 84.7%; Pred. No. 0;  
Matches 2107; Conservative 0; Mismatches 303; Indels 77; Gaps 20;

```

Qy 5 CCCGAGTCTCCGGGTCTGGGATCCACCCGAGG-----CCGGGGAGCCCGCCACAGCCT 59
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1763 CCCGAGTCTCCGGGTCTGGGATCCACCCGAGGATGATCTTGGGAAACCCGCCACAGCCT 1822
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 60 CTACTGGAGAACCCCAAGGCGCTTACC-----AAAATC 96
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1823 GCACCGGAGAGAGCCCAAGTACACTTACCCGGTTTCATTTTCATGTTTAGCCCAAAATTC 1882
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 97 CCGCGGGGTGGGTCCGGGCG-----AGGGGAGGCTGGGTGGGGGGGGGGGAGCCGAGG 152
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1883 CCGCGGGGTGGGTGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1942
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 153 TGGGGGACAGTCTCACACC--TCCAGTGTGATGTTGGCTGGAGCTGGGGTCCGAGGGA 211
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1943 CTGGGGCCAGGGGTTCACACCACATCTAGAGATGTCTGTGGAGCTGGGGGTGGAGCGG 2002
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 212 CCGCTCTCTCCGGGGTATGAAACATATGCTAGATGCAAGATTAATCTGCGCCCTGAA 271
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2003 CCGCTCTCTCCGGGGTATGAAACATATGCTAGATGCAAGATTAATCTGCGCTGAA 2062
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 272 GAGGACCTGCGCTCTGAGCGGACGACACCTGCGCTAGATCTCAAGCCAAAGTGT 331
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2063 GAGGACCTGCGCTCTGAGCGGACGACACATGCGGCTGAGATCAAGCCAAAGTGT 2122
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 332 GAG--GCGGCCAATGTGCTGAACAAAGAGAGCT--ACCTGGAGGGGCAAGTGG--TGA 387
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2123 GAGACTCCGCTTGGAGGAGGAGGAGGAGGCTGAACCTTGAAGGAGGAGATTAATCTGTAAC 2182
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 388 GTGGCTCCACAGATACCTGGAGAAAGGAGAGAGATGCTGACGCGCGGGTACCAAGGG 447
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2183 CGGGCTTCCAGATACCTGGAGAAAGGAGAGAGATGCTGACGCGCGGGTACCAAGGG 2242
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 448 CAGTGGGGGCTCTCCGATCTCTGTAGACCTCTACGCTG--CCTACACAAAGAGAG 506
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2243 CCAGCGGGGCTCTCCGATCTCTGTAGACCTCTACGCTG--CCTACACAAAGAGAGAG 2302
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 507 GAGGAAATGGGACCAACACTAGATATGCGCCCTGCTGTGCTCTGAGGGAGAGATATC 566
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2303 GAGGAAATGGGACCAACACTAGATATGCGCCCTGCTGTGCTCTGAGGGAGAGATATC 2362
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 567 CTCGCGGGTTCGAGATCTCTGTACAGAGATATCTGTGAGGGCGGCTCTCTCTCTG 626
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2363 CTCGCGGGTTCGAGATCTCTGTACAGAGATATCTGTGAGGGCGGCTCTCTCTCTG 2422
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 627 GACAAATTAAGGATGAATCTGTAGGAGTGAAGGAGAGACATCCCTGGAAGACTGA 686
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2423 GACAAATTAAGGATGAATCTGTAGGAGTGAAGGAGAGATCCCTGGAAGACTGA 2481
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 687 TCAGGGGTTCCCTTGTAC-----CCACAGCAGCTTGGCACAGGACTTTTCCCTGAG 741
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2482 TCAGGGGTTCCCTTGTAC-----CCACAGCAGCTTGGCACAGGACTTTTCCCTGAG 2541
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 742 GCGTTGTTCTGCTCTCAC--TCAATGTGTGAGGGGTGAGCTCAGCTCTCTGAGT 800
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2542 GCGTTGTTCTGCTCTAACACTTAATGTGTGAGGGGTGAGCTCAGCTCTCTGAGT 2601
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 801 CCGTTGGCTCAGCTCAGAGTCAAGCCGAGAGTCCCTGCTCCCGCTCAGAGACTAGAA 860
      ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 2602 CCTCAGCCTCCACATCAGCTCAGGACCAAGATCGCTGTTCCCTC-TTCAGGAGCTAGAA 2660  
 QY 861 CTTTCCAGAGAAATAGAGATATATCCAGGTGCCGTGTCAGAGGCTGTCTGGGTCTCG 920  
 Db 2661 TTTTCCAGAGAAATAGAGATATATCCAGGTGCCGTGTCAGAGGCTGTCTGGGTCTCG 2720  
 QY 921 TGTCTCCCTCCACCCAGGATATCTGTCATTTCTTAGAGGTGCATATCCAGGTCG 980  
 Db 2721 TGTCTCCCTCCACCCAGGATATCTGTCATTTCTTAGAGGTGCATATCCAGGTCG 2778  
 QY 981 CTGAGATGTCCTCATGAGATAGCAAGTCTGTAATTTCTGACTCTCTTCAGACCC 1040  
 Db 2779 GAGAGATGTCCTCATGAGATAGCAAGTCTGTAATTTCTGACTCTCTTCAGACCC 2838  
 QY 1041 CCCCAGACACATGACATCCACACCCCTGTCTTGTAGTACAGGACCCCTGAGTCG 1100  
 Db 2839 CCCCAGACACATGACATCCACACCCCTGTCTTGTAGTACAGGACCCCTGAGTCG 2898  
 QY 1101 GGCCTGAGCTTCTACCTCTGCGAGATCATATGACCTGGCAGCGGATGGGAGACCA 1160  
 Db 2899 GGCCTGAGCTTCTACCTCTGCGAGATCATATGACCTGGCAGCGGATGGGAGACCA 2958  
 QY 1161 GACCAGACGTCGAGCTCTGAGACAGGCTGCGAGGAGTGAACCTTCAGAAAGTG 1220  
 Db 2959 GACCAGACGTCGAGCTCTGAGACAGGCTGCGAGGAGTGAACCTTCAGAAAGTG 3018  
 QY 1221 GGCAGCTGTGTGCTGCTTCTGAGAGAGGACAGATACAGTGCATGTGCACATGA 1280  
 Db 3019 GGCCTGTGTGCTGCTTCTGAGAGAGGACAGATACAGTGCATGTGCACATGA 3078  
 QY 1281 GGGGCTGCGGAGCCCTCATGCTGAGATGAGATGAAGGAGAGATGAGGAGATATGTC 1340  
 Db 3079 GGGCTGTGCGGAGCCCTCATGCTGAGATGAGATGAAGGAGAGATGAGGAGATATGTC 3138  
 QY 1341 TGTAGGAGAAAGGAGGAGGCTCTGAGAGCTTAAAGGAGGCTGAGTGGTGGGCTGG 1400  
 Db 3139 TTTTAGGAGAAAGGAGGAGGCTCTGAGAGCTTAAAGGAGGCTGAGTGGTGGGCTGG 3178  
 QY 1401 GGTGAGAGACCTCTACCTCTACCTCTTCCAGAGACAGTCTTCCCTGCCACACATCCG 1460  
 Db 3179 GGTGAGAGACCTCTACCTCTACCTCTTCCAGAGACAGTCTTCCCTGCCACACATCCG 3238  
 QY 1461 ATCAGGAGTATGCTGTGCTGCGCGGTGCTGCTGAGCTGTAGTCTACGACCTGCGTC 1520  
 Db 3239 ATCAGGAGTATGCTGTGCTGCGCGGTGCTGCTGAGCTGTAGTCTACGACCTGCGTC 3298  
 QY 1521 GCTGCTGTGCTGTGAGAAAGAGAGCTCAGTGAAGAGGAGTGAACAAGTGGGCTGGA 1580  
 Db 3299 GCTGCTGTGCTGTGAGAGAGAGAGCTCAGTGAAGAGGAGTGAACAAGTGGGCTGGA 3358  
 QY 1581 GTTTCTGTGCTGCTGCGGAGGTTTCAAGCCCGAGTGAAGTGTGCGGCTGCTGCTACT 1640  
 Db 3359 GATTCTGTGCTGCTGCGGAGGTTTCAAGCCCGAGTGAAGTGTGCGGCTGCTGCTACT 3418  
 QY 1641 GGGAGACACATCCACATCAAGGAGGCTTACCCAGGCTGAGGCTGTGTGCCAGACCTTC 1700  
 Db 3419 GGGAGAGACACATCCACATCAAGGAGGCTTACCCAGGCTGAGGCTGTGTGCCAGACCTTC 3478  
 QY 1701 TCTTTTGAAGACACCTGTGTGACATGAAGAGAGATTTATTAAGTATGATGAAGGA 1760  
 Db 3479 TCTTTTGAAGACACCTGTGTGACATGAAGAGAGATTTATTAAGTATGATGAAGGA 3538  
 QY 1761 TGGGAGCTGATCCAGTAAATCAAGGTGAGAGAGTCCCTGCTGAGAGACACCTTC 1820  
 Db 3539 TGGGAGCTGATCCAGTAAATCAAGGTGAGAGAGTCCCTGCTGAGAGACACCTTC 3598  
 QY 1821 AGGAGAGAGTGTGAGAGAGGACCATCTGCTTCTGTTCTGTTTCTGATATGAGTGA 1878  
 Db 3598 TGGAGAGAGTGTGAGAGAGGACCATCTGCTTCTGTTCTGTTTCTGATATGAGTGA 3655  
 QY 1879 GGTCTGAGTACACATTTCTGAGAACTTCTGAGAGGCTCCAGACATGAGAGGTCTCTTA 1938  
 Db 3656 GGTCTGAGTACACATTTCTGAGAACTTCTGAGAGGCTCCAGACATGAGAGGTCTCTTA 3715

QY 1939 GGAACCTCAGGCCCTGACCAC-CTTTCTGGCCCTTCACAGACGACATTTCTCCACAGATT 1997  
 Db 3716 GGAACCTTAAAGGCCCTGACCACCTTCTGATCTCAGAGGACATTTCTCCACAGATA 3775  
 QY 1998 GAAAGAGAGGAGTACTCTCAGGCTGCAAGTAAATGATGAAGAGGCTGATCCCTGAT 2057  
 Db 3776 GAAAGAGAGGAGTACTCTCAGGCTGCAAGTAAATGATGAAGAGGCTGATCCCTGAT 3835  
 QY 2058 CCTGGGATCTGTGTGTGGGAG-CCATGGGGAGCTCACCACCCACCAATTCCTCTC 2116  
 Db 3836 CCTGGGATCTGTGTGTGGGAG-CCATGGGGAGCTCACCACCCACCAATTCCTCTC 3895  
 QY 2117 TGGCCATCTCTCTGAGTCTGACACAGTGTCTGTTTGTCTACTGAGGAGGAGAC 2176  
 Db 3896 TACCACATCTCTGAGTCTGACACAGTGTCTGTTTGTCTACTGAGGAGGAGAC 3955  
 QY 2177 AGTGCCAGGCTCTAATGTCTCTACAGGCTGTGAATGTGACACCCGGGGGCTG 2236  
 Db 3956 AGTGCCAGGCTCTAATGTCTCTACAGGCTGTGAATGTGACACCCGGGGGCTG 4015  
 QY 2237 ATGTGTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2296  
 Db 4016 ATGTGTGTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4075  
 QY 2297 TCAATGATGAGCATGTGATGGCTGTTTAAAGTGTACACCCCTGAGTGTGATG 2356  
 Db 4076 TGAATGATGAGCATGTGATGGCTGTTTAAAGTGTACACCCCTGAGTGTGATG 4135  
 QY 2357 AATTGTGATGATAA-TTTTCTGTAGTGTGAAGACGTCGCCCTGTGGAGAGT 2414  
 Db 4136 AATTGTGATGATAA-TTTTCTGTAGTGTGAAGACGTCGCCCTGTGGAGAGT 4195  
 QY 2415 GGCAGATTGTGTGATGCTTCCCTT 2441  
 Db 4196 GGCAGATTGTGTGATGCTTCCCTT 4222

RESULT 12  
 PCT-US01-01328-573  
 ; Sequence 573, Application PCT/US0101328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc., et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: P118PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US01/01328  
 ; PRIORITY FILING DATE: 2001-01-17  
 ; Prior application data removed - consult P118 or file wrapper  
 ; NUMBER OF SEQ ID NOS: 927  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 573  
 ; LENGTH: 3098  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; PCT-US01-01328-573

Query Match 63.6%; Score 1554; DB 1; Length 3098;  
 Best Local Similarity 82.5%; Pred. No. 0;  
 Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20;

QY 1 TACTCCGAGTCTCGGGTCTGATCCACCCCGAGGACCGGGAGACCCGACACCTTC 60  
 Db 561 TCCCTAGAGTCTCGGATCGCAATCTACCCCGAGGAGCGGGAGACCCGACACCTTC 620  
 QY 61 TACTCCGAGTCTCGGGTCTGATCCACCCCGAGGACCGGGAGACCCGACACCTTC 98  
 Db 621 TCCCTAGAGTCTCGGATCGCAATCTACCCCGAGGAGCGGGAGACCCGACACCTTC 680  
 QY 99 CGGAGTGTGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 158  
 Db 681 CGGAGTGTGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 739  
 QY 159 CAGGTCTCAGACCTCCAGTGTGATGCTGCTGAGACCTGGGGTCCGAGAGGCTCC 218



Db 740 TAGGGCTCTCACACCCCTCCAGAGGAATGATGGCGACATGGGGCCCGAGCGAGCCCTCC 799  
Qy 219 TCCGCGGGTATGAAACGATATGCTACGATGGCAAGGATTAATCTCCGCTGAAACGAGACC 278  
Db 800 TCCCGGGGATACACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 859  
Qy 279 TGGCGTCTGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 338  
Db 860 TGGCGTCTGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 919  
Qy 339 CCAATGTCGCTGAACAAGAGAGAGCTTACCTGGAGGACGACGACGACGACGACGACGACGAC 398  
Db 920 AGGAATATGAG 979  
Qy 399 GATACCTGGAG 458  
Db 980 GATACCTGGAG 1038  
Qy 459 CTCCCTGATCTCTGATGACCTCTGACCTGACACAGAGAGAGAGAGAGAGAGAGAGAGAG 518  
Db 1039 CTTCCTATCTCTGATGATCTCTGAGATGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAG 1098  
Qy 519 ACCAAGCTGAAATATGAG 578  
Db 1099 CCAATGCTGAGATATGAG 1158  
Qy 579 CAGATCTGATACAGAGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638  
Db 1159 GAGATCCGGTACAG 1218  
Qy 639 ATGAAGTCTGAG 698  
Db 1219 ATGAATTTTGAAG 1277  
Qy 699 TTTGA-CCCAACAG 757  
Db 1278 TTTGAGGAG 1337  
Qy 758 CACATCAATGATGATGAG 817  
Db 1338 CACATCAATGATGATGAG 1387  
Qy 818 GGTCAAG 877  
Db 1388 GGTCAAG 1446  
Qy 878 GATTAATCCAG 937  
Db 1447 GATTTTCCAG 1506  
Qy 938 CAGTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997  
Db 1507 CAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1564  
Qy 998 AGATCAAG 1057  
Db 1565 GAGTCAAG 1621  
Qy 1058 CCCAG 1117  
Db 1622 CCCAG 1681  
Qy 1118 CCGGAG 1177  
Db 1682 CCGGAG 1741  
Qy 1178 TCGTGAG 1237  
Db 1742 TGTGTGAG 1801  
Qy 1238 CTTTGGAG 1297

Db 1802 CTCCTGAGAGAGAGAGAGAGAGATACATGATGACAGAGAGAGAGAGAGAGAGAGAGAG 1861  
Qy 1298 TCATGCTGAG 1339  
Db 1862 TCATGCTGAG 1921  
Qy 1340 CTTTGAAG 1399  
Db 1922 TTTTGAAG 1981  
Qy 1400 GGGTGAAG 1459  
Db 1982 AGATGAG 2041  
Qy 1460 CACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1519  
Db 2042 CACATGAG 2101  
Qy 1520 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579  
Db 2102 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160  
Qy 1580 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1639  
Db 2161 AGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220  
Qy 1640 TGGAG 1699  
Db 2221 TGGAG 2280  
Qy 1700 CTTTGTGAAG 1759  
Db 2281 CTTTGTGAAG 2340  
Qy 1760 ATG--GGAGCTGATCCAGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1816  
Db 2341 GATATGAG 2400  
Qy 1817 CTTTGAAG 1874  
Db 2401 CTTTGAAG 2460  
Qy 1875 CTTGAG 1934  
Db 2461 CTTGAG 2520  
Qy 1935 TCTAG 1994  
Db 2521 TCTAG 2580  
Qy 1995 ATTGAAG 2054  
Db 2581 ATTGAAG 2639  
Qy 2055 GATCTTGGAG 2113  
Db 2640 GATTTTGGAG 2699  
Qy 2114 CTTTGGAG 2173  
Db 2700 -----TACCAACATCTGAG 2753  
Qy 2174 GACAGTCCAG 2228  
Db 2754 GACAGTCCAG 2813  
Qy 2229 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2285  
Db 2814 GGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2873  
Qy 2286 TTTCTTTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2345  
Db 2874 TTTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2933





us-09-622-846-16.rpm

Page 19

Db	2221	TGGGAAGCACCACTCCACACTCATGCGGTCTACCCAGCCCTGGGCGCTGTGTGCCAGCACTTA	2280
Qy	1700	CTCTTTTGTAAAGCACCTGTGACAAATGAAGGACAGATTTTATTTACCTTCATGATTTGTAGTG	1759
Db	2281	CTCATTTGTAAACCTCCTCTGAAATAATGAAGGACACATTTCTTCACCTGCATGATTTATGTG	2340
Qy	1760	ATC--GGGACCTGATCCCAAGTATACAGGTGA--GGAGAGSTCCCTGGGCTAAGACAGA	1816
Db	2341	GTGATGGGACCTGATCCCAAGCAATATACAGGGGAAGGTCCCTGCTGATGACAGA	2400
Qy	1817	CCCTAAGAGGGGACGTTGGTGGAGAGCCACATCTGCTTTCCCTGTTTCTGTATC--GC	1874
Db	2401	CCCTAGAGGGGACGTTGGTGGAGAGCCACATCTGCTTTCTTCATATTTCTGATTCCTGC	2460
Qy	1875	CCCTGGCTCTGCACTCACACATTTCTGGAACCTTCTGAGAGGTCCAAGACTAGAGGTTCC	1934
Db	2461	CCCTGGATCTACAGTTACACTTTCTTGGAACCTTCTCTGGGATCAAGACTAGAGGTTTGC	2520
Qy	1935	TCTAAGACCTCATTGCGCCCTCCACCTTCTTGCGCTCTCCACAGACATTTTCTTCCACAG	1994
Db	2521	TCTAAGACCTTATAGCCCTCCCTCTCTTCTGGGCTCTCCAGAGACATTTTCTTCCCATAG	2580
Qy	1995	ATTGAAGAAGGAGGAGCTACTCTCAGGCTGCAAGTAAATATAGAGAGGCTGATCCCTGA	2054
Db	2581	ATTGAAGAAGGAGGAGCTACTCTCAGGCTGCAAGTAAATATAGAGAGGCTGATCCCTGA	2639
Qy	2055	GATCCTTGGGATCTTGTGTTTGGGAGCC--ATGGGGAGAGTCAACCCCAACCAATTCCTC	2113
Db	2640	GATTTTGGGATTTGTGTGTGACAGCTTATGAGGAGGAGCTCAACCCCAACCAAGTTCTC	2699
Qy	2114	CTCTGGGCACATCTCTGCTGCTGTACACAGGCTGCTTTTGTCTTACTCTAGACAGT	2173
Db	2700	-----TAGCCACATCTGTGGGCTGTGACAGGCTCCTGTTTGTCTTACCCCAATCACT	2753
Qy	2174	GACAGTCCCAAGGCTCTAATGTGTCTCTACAGGCTTGTAAATGTGACACCC-----CGG	2228
Db	2754	GACAGTCCCAAGGCTCTGAGGCTGTCTCTACAGCTAATTAAGATGACACTCCAGGCGAG	2813
Qy	2229	GGGGCTCATGCTGTGTGGGTGTGAGAGGG---AACAGGGGACATAGCTGTGCTATGAGG	2285
Db	2814	GGGGCTCATGCTGTGTGGGTGTGAGAGGG---AACAGGGGACATAGCTGTGCTATGAGG	2873
Qy	2286	TTTCTTTGACTTCAATGATATTAGACATGTGATGGGCTGTTTAAAGTGTACACCCCTCACTG	2345
Db	2874	TTTCTTTGACTTGTGATGCTTGTGACATGAATAGGCTATTTAAGATGTACTCCCTCACAG	2933
Qy	2346	TCACGATATCAATTTGTTGTCATGSAATTTTT--TCTGTAGTGTGAACACAGCTGCCCTGTG	2404
Db	2934	TCACGATATCAATTTGTTGTCATGSAATTTTTTTCTCTATAGTGTGACAGACTTCCTTGTGT	2993
Qy	2405	GGGACTGAGTGGCAGATTT 2424	
Db	2994	GGGACTGAGAGCAAGATAT 3013	
RESULT 14			
PCT-US01-01334-10456			
Sequence 10456, Application PC/TUS0101334			
GENERAL INFORMATION:			
APPLICANT: Human Genome Sciences, Inc., et al.			
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
FILE REFERENCE: PC010PCT			
CURRENT FILING DATE: 2001-01-17			
PRIOR APPLICATION NUMBER: 60/179,065			
PRIOR FILING DATE: 2000-01-31			
PRIOR APPLICATION NUMBER: 60/180,628			
PRIOR FILING DATE: 2000-02-04			
PRIOR APPLICATION NUMBER: 60/214,886			
PRIOR FILING DATE: 2000-06-28			
PRIOR APPLICATION NUMBER: 60/217,487			
PRIOR FILING DATE: 2000-07-11			
PRIOR APPLICATION NUMBER: 60/225,758			
PRIOR FILING DATE: 2000-08-14			
PRIOR APPLICATION NUMBER: 60/220,963			
PRIOR FILING DATE: 2000-07-26			
PRIOR APPLICATION NUMBER: 60/217,496			
PRIOR FILING DATE: 2000-07-11			
PRIOR APPLICATION NUMBER: 60/225,447			
PRIOR FILING DATE: 2000-08-14			
PRIOR APPLICATION NUMBER: 60/218,290			
PRIOR FILING DATE: 2000-07-14			
PRIOR APPLICATION NUMBER: 60/225,757			
PRIOR FILING DATE: 2000-08-14			
PRIOR APPLICATION NUMBER: 60/226,868			
PRIOR FILING DATE: 2000-08-22			
PRIOR APPLICATION NUMBER: 60/216,647			
PRIOR FILING DATE: 2000-07-07			
PRIOR APPLICATION NUMBER: 60/225,267			
PRIOR FILING DATE: 2000-08-14			
PRIOR APPLICATION NUMBER: 60/216,880			
PRIOR FILING DATE: 2000-07-07			

;; PRIOR APPLICATION NUMBER: 60/236,367  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/237,039  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,038  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/236,370  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/236,802  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,037  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,040  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/240,960  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/239,935  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: 60/239,937  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: 60/241,787  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,474  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/246,532  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/249,216  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,210  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/226,681  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/225,759  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/225,213  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/227,182  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/225,214  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/235,836  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/230,438  
;; PRIOR FILING DATE: 2000-09-06  
;; PRIOR APPLICATION NUMBER: 60/215,135  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: 60/225,266  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/249,218  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,208  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,213  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,212  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,207  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,245  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,244  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,217  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,211  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,215  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,264  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,214  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,297

;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/232,400  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/231,242  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,081  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,080  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,414  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,244  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,064  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/233,063  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,397  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,399  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,401  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/241,808  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,826  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 63.6%; Score 1554; DB 1; Length 3098;  
Best Local Similarity 82.5%; Pred. No. 0;  
Matches 2047; Conservative 0; Mismatches 350; Indels 83; Gaps 20;

OY 1 TACCTCGAGTCTCCGGGCTGTGGATCCACCCGAGGCGGGAGCCGACACCTTC 60  
DB 561 TCCCTCAGAGTCTCGGATCGGAATCTACCCGAGGACCGCCGACACCTTC 620  
OY 61 TACCTGGAGAACCCCAAGGCGCTTTA-----CCAAATCCC 98  
DB 621 CACCCGGGAGAGTCCCGAGGCTTTACCCAGGTTCATTTCAGTTTAGCCCAATCCC 680  
OY 99 CGCGGCTGGGTCGGGCGGAGGCGAGGCTCGTGCGGGGCTGACCCGAGGGGTGGGC 158  
DB 681 CGCGGCTGGGCGGAGGCGGAGGCTCGTGCGGGGCTGAGCTG-CGGGACCGGC 739  
OY 159 CAGGTTCTCACACCTTCAGTGTGATGCTGCACCTGGGGTCCGAGGACGCTTC 218  
DB 740 TAGGCTCTCACACCTTCAGGGAATGATGCTGCACTGGGGCCCGACGACGCTTC 799  
OY 219 TCCGCGGTATGACAGTATGCTTACGATGCGAAGGATTACCTCGCCCTGAACGAGACC 278  
DB 800 TCCCGGGTATACACAGCAGCTGACGAGGCAAGGATTACATCTCCCTGAACGAGACC 859  
OY 279 TCGGCTCTGAGCCGAGCGGACATGCGGCTTGAATCTCCAAAGGCAAGTGTGAGGG 338  
DB 860 TCGGCTCTGAGCCGAGCGGACATGCGGCTTGAATCTCCAAAGGCAAGTGTGAGGG 338  
OY 339 CCAATGTGCTGAACAAGAGAGCTTACCTGAGGCGCAGTGCAGTGTGCTTCACA 398  
DB 920 AGGAATATGAGAGAGTGTAGAGACCTACTGAGAGCGCAGTGCAGTGTGCTTCACA 979  
OY 399 GATACCTGAGAAACGGAGAGAGATCTGAGCGCGGCTACCAAGGGCAGTGGGGCGC 458  
||||| ||||||| ||||||| ||| ||||||| ||||||| ||| |||||||





Fri Jan 31 06:07:01 2003

us-09-622-846-16.rpm

Page 23

QY	1935	TCGAGACCTATGAGCCCTGCACACTTTGTGGCCCTCAGACGACATTTTCCTCCACAG	1994
Db	2521	TCTAGACCTTATGCCCCCTGCTCCTTTTGTGGCCTCAGACGACATTTTCCTCCACAG	2580
QY	1995	ATTGAAAAGAGGAGAGCTACTCTCAGGCTGCAGTAATGATGAGAGGCTGATCCCTGA	2054
Db	2581	ATTGAAAAGAGGAGAGCTACTCTCAGGCTGCAGTAATGATGAGAGGCTGATCCCTGA	2639
QY	2055	GATCCCTGGGAGATCTGTGTGTGGGAGCC-ATGAGGAGACTACCCACCCACAATTCGTC	2113
Db	2640	GATTTGTTGGGATATTGTGTGTGTCAGAGACCTATAGGAGACTTACCCACCCACAATTCCTC	2699
QY	2114	CTCTGGCCACATCTCTCTGTGCTCTGCACAGAGTCTGTTTTTGTCTACTAGGCAAT	2173
Db	2700	-----TACCACACATCTGTGGGCTCTGACACAGTCTCTGTTTTTGTCTACCCACAATCT	2753
QY	2174	GACAGTGGCCACAGGCTCTAATGTGTCTCAGGCTGTAAATGTGACACCC----GGG	2228
Db	2754	GACAGTGGCCACAGGCTCTGGGGGTCTCTCTCAGCTAATTAAGTGTGACACTCAGGGCAG	2813
QY	2229	GGGGCCCTGATGTGTGTGTGGTGTGTGAGGGG---AACAGGGGACATTAAGTGTGATAGG	2285
Db	2814	GGGCCCTGATGTGATGTGGGGTGTGGGGGGGAACAGAGGACATCACTGTGCTATTGGG	2873
QY	2286	TTTCTTGTACTTCATATGATATTGAGACATGTGATGGGCTGTTTAAGTGTACCCCTCAGG	2345
Db	2874	TTTTCTTGTACTTGGATGTCTTGAGACATGAATATGGGCTATTTAAGTGTACCTCTCAGG	2933
QY	2346	TGACTGATATGAAATTTGTCTATGAAATATTTT-TCGTAGTGTGAAACAGCTGGCCCTGT	2404
Db	2934	TGACTGATATCGAAATTTGTCTATGAAATATTTTCTCTAATAGTGTGAGACAGCTTCCCTGT	2993
QY	2405	GGGACTGAGTGGCAAGATTT 2424	
Db	2994	GGGACTGAGGAAAGCAAGATAT 3013	

Search completed: January 31, 2003, 02:13:24  
Job time : 4838 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

```
Run on: January 30, 2003, 22:22:43 ; Search time 341 Seconds
        (without arguments)
```

8127.015 million cell updates/sec

Title: US-09-622-846-16  
Perfect score: 2442

Sequence: 1 tactcccgagtcctccggtc.....tgttcatgccttccttg 2442

Gapop 10.0 , Gapext 1.0

Searched: 2475311 seqs, 567426730 residues

Total number of hits satisfying chosen parameters: 4950622

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database ::

```

1: Pending_Petents_VA_New: *
2: /c9n12_6.pdataa1/pna/PCT_NEW_COMB.seq: *
3: /c9n12_6.pdataa1/pna/us06_NEW_COMB.seq:
4: /c9n12_6.pdataa1/pna/us07_NEW_COMB.seq:
5: /c9n12_6.pdataa1/pna/us08_NEW_COMB.seq:
6: /c9n12_6.pdataa1/pna/us09_NEW_COMB.seq:
7: /c9n12_6.pdataa1/pna/us10_NEW_COMB.seq:
8: /c9n12_6.pdataa1/pna/us10_NEW_COMB.seq:
9: /c9n12_6.pdataa1/pna/us10_NEW_COMB.seq:

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1551.6	63.5	4316	6	US-10-257-021-81	Sequence 81, App1
2	461.2	18.9	466	6	US-10-203-138A-753	Sequence 753, App1
3	461.2	18.9	466	6	US-10-203-138A-754	Sequence 754, App1
4	408.8	16.7	412	6	US-10-203-138A-4873	Sequence 4873, App1
5	374.8	15.3	467	6	US-10-203-138A-2488	Sequence 2488, App1
6	363	14.9	478	6	US-10-203-138A-751	Sequence 751, App1
7	348.8	14.3	470	6	US-10-203-138A-2178	Sequence 2178, App1
8	337.4	13.8	465	6	US-10-203-138A-752	Sequence 752, App1
9	319.4	13.1	1400	6	US-10-085-198-67	Sequence 67, App1
10	305	12.5	305	6	US-10-203-138A-99804	Sequence 99804, App1
11	300.8	12.3	446	6	US-10-203-138A-1820	Sequence 1820, App1
12	300.4	12.3	453	6	US-10-203-138A-4625	Sequence 4625, App1
13	266.2	10.9	1159	6	US-10-085-198-71	Sequence 71, App1
14	264.4	10.8	4158	6	US-10-152-919A-537	Sequence 537, App1
15	251.8	10.3	301	6	US-10-203-138A-7291	Sequence 7291, App1
16	245.2	10.0	1266	1	PCT-D502-14342-31	Sequence 31, App1
17	245.2	10.0	1266	6	US-10-138-588-31	Sequence 31, App1
18	241.2	9.9	620	6	US-10-310-673-1013	Sequence 1013, App1
19	239.6	9.8	1098	6	US-10-173-138A-46	Sequence 46, App1
20	239.6	9.8	1167	6	US-10-325-999-9260	Sequence 9260, App1
21	239.6	9.8	1568	6	US-10-276-811-533	Sequence 533, App1
22	234	9.6	1225	6	US-10-085-198-69	Sequence 69, App1
23	224.8	9.2	276	6	US-10-334-488-23	Sequence 23, App1
24	224.8	9.2	276	6	US-10-334-488-73	Sequence 73, App1
25	224	9.2	1600	6	US-10-276-781-276	Sequence 276, App1
26	223.6	9.2	3803	6	US-10-152-919A-553	Sequence 553, App1

C	27	215.8	8.8	474	6	US-10-310-673-1044	Sequence 1044, App
	28	211.1	8.6	461	6	US-10-303-138A-2440	Sequence 2440, App
	29	210.4	8.6	276	6	US-10-334-488-75	Sequence 75, App1
	30	208.8	8.5	1540	6	US-10-152-319A-1522	Sequence 1522, App
	31	206.4	8.5	1592	6	US-10-301-856-802	Sequence 802, App1
	32	205.8	8.4	553	6	US-10-310-673-277	Sequence 277, App1
	33	199.8	8.1	426	5	US-09-520-607B-628	Sequence 628, App1
	34	181.2	7.4	582	6	US-10-310-673-1481	Sequence 1481, App1
	35	176.2	7.2	633	6	US-10-310-673-1491	Sequence 1491, App1
	36	160.8	6.6	1130	6	US-10-376-674-413	Sequence 413, App1
C	37	160.2	6.6	587	6	US-10-303-138A-755	Sequence 755, App1
	38	155.4	6.4	439	6	US-10-310-673-106	Sequence 106, App1
	39	153	6.3	439	5	US-09-513-999C-11566	Sequence 11566, App1
C	40	153	6.3	2046	5	US-09-520-312D-169	Sequence 169, App1
	41	115.8	4.7	174	6	US-10-303-138A-5044	Sequence 5044, App1
	42	103.8	4.7	117	6	US-10-303-138A-5903	Sequence 5903, App1
	43	108.8	4.5	347	1	PC11-US02-347A-230	Sequence 973, App1
	44	108.8	4.5	347	1	US-10-283-017-973	Sequence 973, App1
	45	108.4	4.4	435	5	US-09-620-607B-804	Sequence 804, App1

## ALIGNMENTS

```

1 RESULT 1
2 US-10-257-021-81
3 : Sequence 81, Application US/10257021
4 : GENERAL INFORMATION:
5 :
6 : APPLICANT: Morin, Patrice J.
7 :
8 : APPLICANT: Sherman-Baust, Cheryl A.
9 :
10 : APPLICANT: Pizer, Ellen S.
11 :
12 : APPLICANT: Hough, Colleen D.
13 :
14 : TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN
15 :
16 : FILE REFERENCE: 14014.036902
17 :
18 : CURRENT APPLICATION NUMBER: US/10/257,021
19 :
20 : CURRENT FILING DATE: 2002-10-03
21 :
22 : PRIOR APPLICATION NUMBER: PCT/US01/10947
23 :
24 : PRIOR FILING DATE: 2001-04-03
25 :
26 : PRIOR APPLICATION NUMBER: 60/194,336
27 :
28 : PRIOR FILING DATE: 2000-04-03
29 :
30 : NUMBER OF SEQ ID NOS: 147
31 :
32 : SOFTWARE: FASTEDS for Windows Version 4.0
33 :
34 : SEQ ID NO 81
35 :
36 : LENGTH: 4316
37 :
38 : TYPE: DNA
39 :
40 : ORGANISM: Homo sapiens
41 :
42 : US-10-257-021-81

```

Query Match	63.58;	Score 1551.6;	DB 6;	Length 4316;
Best Local Similarity	82.7%;	Pred. No. 0;		
Matches 2052; Conservative	0;	Mismatches 344;	Indels 84;	Gaps 21

QY	1	TATCCCAAGTGTCCGGGGCTGAGGATCCACCCGAGGACCGGAGACCCGACACCTC	60
Db	1377	TCCCCCGAATCTCCGGATCCGAATCTACCCGAGGACGCGAGACCCCTC	14
QY	61	TACCTGGAGAACCCCAAGCGCCCTTTA-----CCAAATCC	98
Db	1436	CACCCGGAGAGTCCCTCAGGCGGCTTTACGAGGTTCATTTAGGCGCAAAATGCC	145
QY	99	CGCGGGGTGCGGGCGAGGGCGAGGCTCGTGGGCGGGGCTGACCGAGGGGGTGGG	158
Db	1496	CGCGGGTTGGCGCGGAGGGGCGGGGGTACGTGAGCGGGGCTGACGTG-CGGGACCGCG	155
QY	159	CAGGTTCTACACCTCCAGTGGATGATGGCTGCGACTGGGGTCCGACGACGCTCC	218
Db	1555	TAGGTCCTACACCTCCAGGAAAGATGGCTGCGACATGGGGGCCGCGAGACCCCTCC	161
QY	219	TCCGCGGATGACAGATGATGCTTCAGTGGCAGAGATTACTCGCCCTGACGAGGACG	278
Db	1615	TCCGCGGGATATCAGCAGCAGCGGTACAGCGCAAGATTACATCTCCGTGAACGAGGAC	167
QY	279	TGCGGCTCTTGAGCGCAGCGGACACTCGCGGCTAGATCTTCAAGCGCAAGTGTGAGCGG	338

Dp	1675	TGCGCTCTGGACCGCGCGGAGAACCTTGCTGGATACCCAGCCTTCTATGAGGAG	1734
Oy	339	CCAAATGGCTGAAACAAGACAGACCTACCTGAGAGCAGCTGCGTGGAGTGGCTCCACA	398
Dp	1735	AGGAATATGCAAGAGAGATTTCAGGACCTTACCTTGAGAGCGGAGATGGCTGTGGATTGCTCCGCA	1794
Oy	399	GATTAACCTGGAGAGGAGAGAGATCTTCACACCGCGCGGTGATCAGAGGGGAGTGGGGCGC	458
Dp	1795	GATACCTGGAGAAAGGAGAGAGAACCTTCACACGCGCAGTACAGGAGGCCAT - GSGGCG	1853
Oy	459	CTCCCGATCTCTGTGAGACCTCTCAGCCCTGGCCCTAGACAGGAAGAGAGGAAATATGG	518
Dp	1854	CTTCCCTATCTCTGTGATCTCTTGGATGGGCTTCGCACAGATTGGGAGGAAATGGG	1913
Oy	519	ACCAACACTAGAAATATGCGCCCTCTGTGCTGAGGAGAGATCTCTGGGTTTC	578
Dp	1914	CCCAATGCTAGGAATATGGCCCTCCCTAGTCTTGAGTAAAGAAATATCTTCGCGCTTTC	1973
Oy	579	CAGATCTGCTACCAAGAGATATTCGAGAGGCGCGCTCTGCTCTGAGGACAATTAAGG	638
Dp	1974	GAAATCCGGTACCAAGAGATGATGAGAGTCCGCCCTCTCTCTGAGGACAATTAAGG	2033
Oy	639	ATGCAAGTCTGAGAGAGTGGAGGAGACACATCCCGGAAGACATGATCAGGGGTCC	698
Dp	2034	ATGAATCTCTGAGGAGATGGA - GGGAAATGCTCCCTGGATACGATCCGGGCTCC	2092
Oy	699	TTTGA - CCCCAAGCACTTGGCCACCAAGACTTTTCCCTGACGCCCTGTCTGCT	757
Dp	2093	TTTGAACCCCTCCAAAGACGCTTGGGCCCGCTGACTTTCTCCAAAGTTGTGCTCTGCT	2152
Oy	758	CACACTATGCTGTGGGGGTGACTCTCAGCTCTGTAGTCCCTTGGCCCTCACATCA	817
Dp	2153	CACACTATGTTGGGGCTGTGAATCC - - - - - AGTCCCGGCTCCACCTTA	2202
Oy	818	GGTGAAGACCGGAGAGTCCCTGTGCCCCCGCTGAGAGATGAATTTCCAAAGAAATAGA	877
Dp	2203	GGTGAAGAGCCAAAGACTCCCTGCT - CCCCACTAGAGATCGAACTTTCCAAAGAAATAGA	2261
Oy	878	GATTATCCAGAGTCCGCTGCTCAGGCTGTGTCTGTGCTCTGCTCCCTTCCACCC	937
Dp	2262	GATTATCCAGAGTCTGTGTCTCAGGCTGTGTCTGGGTTCTGTGCTCCCTTCCACCC	2321
Oy	938	CAGATCTGTGATTTCTTGAATGATGATACATTCAGATGCTGCTGTGAGTGTCCATGAG	997
Dp	2322	CAGATCTGTGATTTCTTGAATGATGATACATTCAGATGCTGCTGTGAGTGTCCATGAG	2379
Oy	998	AGATGAAGATGCTTGAATTTCTGTGACTCTCTTGAAGACCCCGCCAAACACACATGGA	1057
Dp	2380	GAGTGAAGATGCTTGAATTTCTGTGACTCTCTTGAAGATCTTGAAGACCCCGCCAAACACATGGA	2436
Oy	1058	CCCAACACCTGTCTTGAATTAAGGACACCTGAGGTGTGGGCCCTTGGGCTTCTAC	1117
Dp	2437	CCCAACACCTGTCTTGAATTAAGGACACCTTGAAGGTGTGGGCCCTTGGGCTTCTAC	2496
Oy	1118	CTGCGAGATCTTACTGTGACCTGGCAGCAGGAGTGGGAGAGCAACACCAAGATGTGAGG	1177
Dp	2497	CTGCGAGATCTTACTGTGACCTGGCAGCAGGAGTGGGAGAGCAACACCAAGATGTGAGG	2556
Oy	1178	TGCTGGAAGACAGGCTCTGACAGGAGATGAACTTCCAAATGGGAGGCTGTGTGTGTG	1237
Dp	2557	TGCTGGAAGACAGGCTCTGACAGGAGATGAACTTCCAAATGGGAGGCTGTGTGTGTG	2616
Oy	1238	CTTCTGAGAGAGAGATAGATAGCTGTCATGTGTCAGACATGAGACGGCTGCGGAGCCCG	1297
Dp	2617	CTTCTGAGAGAGAGATAGATAGCTGTCATGTGTCAGACATGAGACGGCTGCGGAGCCCG	2676
Oy	1298	TCTATGTGATGAGATGAAGAGAGAGAT - - - - - GGAGGATCATGAT	1359
Dp	2677	TCTATGTGATGAGATGAAGAGAGAGAT - - - - - GGAGGATCATGAT	2756
Oy	1340	CTTGTGAGGAAGACAGACCTCTCTGAAGACCTTAAACAGGCTGTGTGAGGCTGTG	1399
Dp	2757	CTTGTGAGGAAGACAGACCTCTCTGAAGACCTTAAACAGGCTGTGTGAGGCTGTG	2816

Dh	2737	TTCTCAGGGAAAGACGAGGCCCTTCTGAGACTCTTCACACAGGTCACAGSCTGAGGCTCG	2798
Oy	1400	GGGTCAGAGACCTCTACCTTACCTCCTCTTCCCAAGACAGCTTCCCTGCCCCACATCC	1459
Dh	2797	AGATCAGGGCCCCCTACCTCCCTCCCTCTCTTCCCAAGACAGCTTCCCAAGCCCCATATCC	2856
Oy	1460	CATCATGGGTATCGTTGCTGGAGCCGCTGTTCTACCTCTACCTCTATGTCAGTGAGCTCGGT	1519
Dh	2857	CATCGTGGGCATCGTGTGCTGGCCCTGTTCTGCTGAGCATCTGTGTCACGTGACATGTGGT	2916
Oy	1520	CGGTGCTGCTGCTGAGAAAGAAAGAGCAGCTAGGAAAGGGGTGCAAGTGGGGCTCG	1579
Dh	2917	CGCTGCTGTGATGTGAGAGAAAGAGCTCAGGT-AGSAAAGGGTGAAGATGAGATCTG	2975
Oy	1580	AGTTTCTCTTCTCCACTGSGGGTTTCAAGCCCCAGGTGAAAGTGTGCTTGCTGCTTC	1639
Dh	2976	AGTTTCTCTTCTCCACTGSGGGTTTCAAGCCCCAGGTGAAAGTGTGCTTGCTGCTTC	3035
Oy	1640	TGGGAAGCACATCCACATCTATGAGGCCATCCAGCCAGCCCTGATGTCAGACACTT	1699
Dh	3036	TGGGAAGCACATCCACATCTATGAGGCCATCCAGCCAGCCCTGATGTCAGACACNA	3095
Oy	1700	CTCTTTTGTAAAGCACCCGTAACATGAAGAGACATATTATTAACCTGATGATGACAG	1759
Dh	3096	CTATATTGTAAAGCTCCCTGTGAAATGAAAGACATTTCTTACCTTGATGATATGATGT	3155
Oy	1760	ATG-GGACCTGATCCCAATATCACAGTCA-GGAGAGTCCCTGCTAAAGACAGA	1816
Dh	3156	GATATGGACCTGATCCCAAGATGACAAATACAGGGGAAAGTCCCTGTGTATGACNA	3215
Oy	1817	CCATTAGAGGCGAGTTGGTGTGAGAGCCACACATCTCTTTCTCTTCTCTGATC-GC	1874
Dh	3216	CCTCAGAGGAGGAGTGTGCTCAGAGCCACACATCTCTTCTCTTCTCTGATCCTG	3275
Oy	1875	CGTGGTCTGACAGTACACATTTCTGGAACCTTCGAGGGTCCAAACATAGAGGTTCC	1934
Dh	3276	CTGAGATCTACAGTTACACTTTCTGTGAACCTTCTGTGGATCAAAACATAGGGGTTCC	3335
Oy	1935	TCTAGACCTCATGGCCCTGACACCTTTCTGGCCTCTCAAGACATTTCTTCCACAG	1994
Dh	3336	TCTAGACCTCATGGCCCTGACACCTTTCTGGCCTCTCAAGACATTTCTTCCCATAG	3395
Oy	1995	ATTGAAAGAGAGGAGCTACTCTCAGGCTGCAAGTAAGTATGAAGAGGCTGATCCCTGA	2054
Dh	3396	ATTGAAAGAGAGGAGGCTACTCTCAGGCTGCAAGTAAG-ATGAAGAGGCTGATCCCTGA	3454
Oy	2055	GATCGTGGGATCTGTGTTTGGGAAGC-ATGAGGAGACCTCACCCACACATTCCTC	2113
Dh	3455	GATTTGTGGGATATTGTGTGAGAGCTCATGAGGAGACTCACCCACACAGTTCTCT	3514
Oy	2114	CTCTGGCCACATCTCTGTGCTCTGACACAGAGTGTCTTTTCTTCTACTCTAGGAGT	2173
Dh	3515	-----TAGCCACATCTCTGTGGCTCTGACCAAGTCTCTTTTCTTCTACCCCAATCATCT	3568
Oy	2174	GACAGTGCCCAAGGGCTCTAAAGTGTCTGCACAGGCTTCTAAATGTGACACCC-----CG	2228
Dh	3569	GACAGTGCCCAAGGGCTCTGAGGCTGTCTCTCACAAGCTAATAAAGGTGACATCCAGGCGAG	3628
Oy	2229	GGGGCGTGAATGTGTGGGTTGTGAGGGG---AACAGGGAGCAATACGTTGCTATGAGS	2285
Dh	3629	GGGGCGTGAATGTGTGGGTTGTGAGGGGGAACAGAGGCACTCACCTTGCTATTGCG	3688
Oy	2286	TTTTCTTGAATCAATGTATTAAGACATGATGAGTGGCTGTTAAAGTGCACCCCTTCACTG	2345
Dh	3689	TTTTCTTGAATCAATGTATTAAGACATGAAAGGGCTATTAAAGTGTACCTCTCAGCG	3748
Oy	2346	TGACTATATGAATTTGTCTAGTAATTTTT--TCTGTATGTGAAGACGTCGCCCTTCA	2404
Dh	3749	TGACTATATCAAAATTTGTCTATGAATATTTCTCTATATGTGTGACAGAGCTTCTGTGT	3808
Oy	2405	GGGACGTGAGTGGCAAGATT 2424	
Dh	3809	GGGACGTGAGAACCAAGAT 3828	





QY	1370	ACCTTAAACAGGCGTGGTGTGAGAGGCTGGGGGCTAGAGACCCCTACCTTCACTCTCTTT	14.29
Db	164	ACCTTTAGCA-----GGGTCAAGGAGCCCTCACTTCCCTCTTTT	125
QY	1430	CCGAGACAGTCTTCCCTGCCACACATCCCATCATGGGTATCGTTCGAGCCGGTGT	148.93
Db	124	CCGAGAGCTGTGTCCAGGACCCACATCCCATCCGTGGGACATATCTGTGGCTGGTCT	65
QY	1490	CCCTGCACCTGTAGTCACTGAGAGCTCGGCTCCCTCTCTGCTGTGGAGAAAGAAAGCTC	154.93
Db	64	CCCTGGAGGCTGTGATCACTAGCTAGCTGTGGTCCCTGCCATGTGGAGGAGGAAAGAGTC	5
QY	1550	AGGT 1553	
Db	4	AGGT 1	

```

RESULT 6
US-10-203-138A-751/c
: Sequence 751, Application US/10203138A
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
: FILE REFERENCE: PB 0004 WO B
: CURRENT APPLICATION NUMBER: US/10/203,138A
: PRIOR FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/6532,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263.5
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/226,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 21 September 2000 (21.09.00)
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15438
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 751
: LENGTH: 478
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AB023056.1
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 17
: US-10-203-138A-751

```

[illegible]

Oy	1252	CAGAGATACAGCTGGCATATGTCACATGAGAGGGGCTCCGGAGGCCCTCATGCTAGAGATAGG	1311
Db	298	CAGAGATACCCCTGGCATATGTCACATGAGAGGGGTTGCCAAGGCCCTCACCCAGAGATGG	239
Oy	1312	AGTAAAGGAGGAGAT-----GGAGGCATCATATGCTGTAAAGGGAAGAGAGAGCTCTC	1364
Db	238	GGTAAAGCGAGGAGATGAGTGGAGGGGGGGCATATGCTCTTAA-GGAAAGCAGAGAGCTCTTC	180
Oy	1365	TGAAAGCTTTAAACAGGGTCTGTCGTAAAGGAGCGTGGGGGTCAGAGAGCCCTCAACCTACCT	1424
Db	179	TGAGAACTTTCAGACAGGGTGGTGTCTGAGGGGCTGAAGGTCAGAGGACCTCAACTTCCCT	120
Oy	1425	CGTTTCCCGAGACATCTTCCCTCCGCCACCACTCATAGGGTATACGTTGTGGGCTCG	1484
Db	119	TTTTTCCCGAGACATCTTCTCAGCCCAACCACTCATATGGGATATCGTTCTGGGCTCG	60
Oy	1485	GTTGCTCTTCAGAGCTATAGTACATGAGAGCTGGGCTCGGCTGTGCTGTGCTGAGAAAGAA	1543
Db	59	GTTCCTCTTCAGAGCTATAGTACATGAGAGCTGGTTCCTGCTGTATGTGACAGAAAGAA	1

```

RESULT 7
US-10-203-138A-2178
: Sequence 2178, Application US/10203138A
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: PB 0004 WO 8
: CURRENT APPLICATION NUMBER: US/10/203.138A
: PRIOR FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263 6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 21 September 2000 (21.09.00)
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15438
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 2178
: LENGTH: 470
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AP000507.1
: OTHER INFORMATION: EXPRESSED IN BT474. SIGNAL = 8
US-10-203-138A-2178

```

	Query Match	14.9%	Score 348.8	DB 6	Length 470
	Best Local Similarity	18.9%	Pred. 3.2e-77		
	Matches 423	Conservative	0	Mismatches 47	Indels 6
				Gaps	4
QY	808	CCCTCACTACGACGACGAGGCGTCCTGCTCCCGCCGACAGACTGAACTTCCCA	867		
DB	1	CCTCACTACGATACGAGCAGCAAGATCCTTG-TTCCCGCGTCAGAGACTGAACTTCCCA	59		
QY	868	AGGAATAGAGAAATTATCCACAGTGTGCCCGTGCAGAGTGATGTGGTGTGTGCTCC	927		
DB	60	ATGAATAGGAGAAATTATCCACAGTGTGCCCTGATC-GCTGTGTGTCTGGGTGTGTGGC-CCC	116		

OY 928 TTCCCAACCCAGATATCTGTCATCTTAGAGTGTACATCGAGTGTGTCAGT 987  
DB 117 TTCCCAACCCAGATATCTGTCATCTTAGAGTGTGTCAGT--GGTGGTCTTAGAGT 174  
OY 988 GTCCATGAGAGATGCAAGTGTGATTTTCTGATCTCTTTCAGAACCCCCCAAG 1047  
DB 175 GTGCATGAGAGATGCAAGTGTGATTTTCTGATCTCTTTCAGAACCCCCCAAG 234  
OY 1048 ACACAGTGAAGCCACACCTGCTTGTGATCTGAGGACACCTGAGTGTGAGCCCTG 1107  
DB 235 ACACAGTGAAGCCACACCTGCTTGTGATCTGAGGACACCTGAGTGTGAGCCCTG 294  
OY 1108 GGCCTTACCTGCGGAGATCATACGACCTGCGGAGATGGGAGAGACCAACCCAG 1167  
DB 295 GGCCTTACCTGCGGAGATCATACGACCTGCGGAGATGGGAGAGACCAACCCAG 354  
OY 1168 GACGTGAGAGCTGTGAGACAGGCTGCGAGGAGATGGAACCTTCCAGAGTGGGACGT 1227  
DB 355 GACGTGAGAGCTGTGAGAGACAGGCTGCGAGGAGATGGAACCTTCCAGAGTGGGACGT 414  
OY 1228 GTGGGTGGCTTCTGAGAGAGAGATCATACGACCTGCGGAGATGGGAGAGG 1283  
DB 415 GTGGGTGGCTTCTGAGAGAGAGATCATACGACCTGCGGAGATGGGAGAGG 470

## RESULT 8

US-10-203-138A-752/c  
; Sequence 752, Application US/10203138A  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DEIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474  
; FILE REFERENCE: PB 0004 WO 8  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/10/203.138A  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207.456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632.366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24253.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236.359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234.687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608.408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 15438  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 752  
; LENGTH: 465  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AB023057.1  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4  
US-10-203-138A-752

Query Match 13.8%; Score 337.4; DB 6; Length 465;  
Best Local Similarity 87.8%; Pred. No. 2.2e-74;  
Matches 403; Conservative 0; Mismatches 51; Indels 5; Gaps 3;  
OY 1400 GGGTCAGAGACCTTACCTTCTTCCAGAGAGATGTCCTGCGCACCATCC 1459  
DB 457 GGGTCAGAGATCCCTTCTTCCAGAGATGTCCTGCGCACCATCC 398

OY 1460 CATCATGGGTATCTGTCGCTGCTGCTTCTTCTGACGTAGTACATCGAGTGTGCT 1519  
DB 397 CATCATGGGTATCTGTCGCTGCTGCTTCTTCTGACGTAGTACATCGAGTGTGCT 338  
OY 1520 CGCTGCTGCTGTCGAGAGAAAGAGCTCAGTAAAGAGAGGAGTGAAGTGGAGTCTG 1579  
DB 337 CGCTGCTGCTGTCGAGAGAAAGAGCTCAGTAAAGAGAGGAGTGAAGTGGAGTCTG 278  
OY 1580 AGTTTCTGTCGCTGCTGTCGAGAGAAAGAGCTCAGTAAAGAGAGGAGTGAAGTGGAGTCTG 1639  
DB 277 AGTTTCTGTCGCTGTCGAGAGAAAGAGCTCAGTAAAGAGAGGAGTGAAGTGGAGTCTG 220  
OY 1640 TGGGAAGACCATTCACACTGATGAGGCTTACCGAGCTGCTGCTGCTGCTGCTG 1699  
DB 219 TGGGAAGACCATTCACACTGATGAGGCTTACCGAGCTGCTGCTGCTGCTGCTGCTG 160  
OY 1700 CTCTTTGTAAGCACCTGTCACATGAGAGACAGATTTATACCTTGATGATGATG 1759  
DB 159 CTCTTTGTAAGCACCTGTCACATGAGAGACAGATTTATACCTTGATGATGATGATG 100  
OY 1760 ATGGGGACCTGATCCAGTATCATACAGTGTGAGAGAGAGTCCCTGCTGCTGCTGCTG 1819  
DB 99 AT-GGACCTGATCCAGTATCATACAGTGTGAGAGAGAGTCCCTGCTGCTGCTGCTGCTG 43  
OY 1820 TAGAGAGCAGTGTGTCGAGAGCCACATCTGCTTCT 1858  
DB 42 CAGAGAGGCGTGTGTCGAGAGCCACATCTGCTTCT 4

## RESULT 9

US-10-085-198-67  
; Sequence 67, Application US/10085198  
; GENERAL INFORMATION:  
; APPLICANT: Alsbjork et al.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-279  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US/10/085.198  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/271.646  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/276.401  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/311.981  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: 60/312.858  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/271.840  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/277.324  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/286.096  
; PRIOR FILING DATE: 2001-04-21  
; PRIOR APPLICATION NUMBER: 60/299.695  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/315.614  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/272.405  
; PRIOR FILING DATE: 2001-02-28  
; Remaining prior Application data removed - See file Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 653  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 67  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-198-67

Query Match 13.1%; Score 319.4; DB 6; Length 1400;  
Best Local Similarity 71.9%; Pred. No. 9.9e-70;  
Matches 524; Conservative 0; Mismatches 76; Indels 129; Gaps 3;  
OY 1033 TCAGACCCCAAGACACAGTACCCACACCTGCTCTTGAATAGAGACACCC-- 1090







```

; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO: 1820
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP00508.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12
US-10-203-138A-1820

```

```

Query Match          12.3%; Score 300.8; DB 6; Length 446;
Best Local Similarity 82.7%; Pred. No. 2.8e-65;
Matches 369; Conservative 0; Mismatches 72; Indels 5; Gaps 2;

```

```

QY 1154 AGGACCAACCCAGACGCTGAGCTCTGAGAGACAGCCCTGAGGGGATGAACTTCC 1213
    1 AGGACCAACCCAGACGCTGAGCTCTGAGAGACAGCCCTGAGGGGATGAACTTCC 60
QY 1214 AGAGTGGGAGCTGTGTGTGCTCTCTGAGAGAGAGATACAGTGCATGTGC 1273
    61 AGAGTGGGAGCTGTGTGTGCTCTCTGAGAGAGAGATACAGTGCATGTGC 120
QY 1274 AGCATGAGGGGCTGCCGAGACCCCTCATGCTAGATGAGATGAGGAGATGAGG 1331
    121 AGCATGAGGGGCTGCCGAGACCCCTCATGCTAGATGAGATGAGGAGATGAGG 180
QY 1332 CATCATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1391
    181 CATCATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 1392 AGGGTGGGGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1451
    241 AGGGTGGGGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 1452 ACCATGCCATCATGAGGATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1508
    301 ACCATGCCATCATGAGGATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 1509 GAGCTGGGCTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
    361 GAGCTGGGCTGCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 1569 AGTGGGGTCTGAGTTTCTTCCCA 1594
    421 AGTGGGGTCTGAGTTTCTTCCCA 446

```

```

RESULT 12
US-10-203-138A-4625
; Sequence 4625, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 MO 8
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312

```

```

; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO: 4625
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO DB4394.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.1
US-10-203-138A-4625

```

```

Query Match          12.3%; Score 300.4; DB 6; Length 453;
Best Local Similarity 80.6%; Pred. No. 3.6e-65;
Matches 390; Conservative 0; Mismatches 61; Indels 33; Gaps 2;

```

```

QY 1113 CTACCCGCGGAGATCATCTGACCTGAGGAGGAGGAGGAGAGAGAGAGAG 1172
    1 CTACCCGCGGAGATCATCTGACCTGAGGAGGAGGAGGAGAGAGAGAGAGAG 60
QY 1173 GAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
    61 GAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 1233 GGTGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
    121 GGTGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 1293 GGGCCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
    181 GGGCCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 1351 AGCAGAGCCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
    241 AGCAGAGCCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 269
QY 1411 CCTACCTTACCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
    270 CCTACCTTACCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
QY 1471 TCGTGTGAGGCTGTGTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530
    330 TCGTGTGAGGCTGTGTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 389
QY 1531 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590
    390 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 449
QY 1591 CCCA 1594
    450 CCCA 453

```

```

RESULT 13
US-10-085-198-71
; Sequence 71, Application US/10085198
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279

```

```

CURRENT APPLICATION NUMBER: US/10/085,198
CURRENT FILING DATE: 2002-02-25
PRIORITY APPLICATION NUMBER: 60/2271,646
PRIORITY FILING DATE: 2001-02-26
PRIORITY APPLICATION NUMBER: 60/276,401
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/311,981
PRIORITY FILING DATE: 2001-08-13
PRIORITY APPLICATION NUMBER: 60/312,858
PRIORITY FILING DATE: 2001-08-16
PRIORITY APPLICATION NUMBER: 60/271,840
PRIORITY FILING DATE: 2001-02-27
PRIORITY APPLICATION NUMBER: 60/277,324
PRIORITY FILING DATE: 2001-03-20
PRIORITY APPLICATION NUMBER: 60/286,096
PRIORITY FILING DATE: 2001-04-21
PRIORITY APPLICATION NUMBER: 60/299,695
PRIORITY FILING DATE: 2001-06-20
PRIORITY APPLICATION NUMBER: 60/315,614
PRIORITY FILING DATE: 2001-08-26
PRIORITY APPLICATION NUMBER: 60/272,405
PRIORITY FILING DATE: 2001-02-28
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 653
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 71
LENGTH: 1159
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-198-71

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:07:33 ; Search time 103 Seconds

(without alignments)  
7270.919 Million cell updates/sec

Title: US-09-622-846-16

Perfect score: 2442  
Sequence: 1 taccctccgagctccgagtc.....tggctatgcctcccttgg 2442

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCPUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/Backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1415	57.9	6553	1 US-08-522-942-1	Sequence 1, Appl
2	426.8	17.5	600	3 US-08-577-081A-3	Sequence 9, Appl
3	340	13.9	587	3 US-08-577-081A-9	Sequence 6, Appl
4	333.8	13.8	575	3 US-08-577-081A-6	Sequence 52, Appl
5	249.2	10.2	544	3 US-08-577-081A-52	Sequence 2, Appl
6	238	9.7	4059	2 US-08-564-313-2	Sequence 1, Appl
7	238	9.7	4059	2 US-08-564-313-1	Sequence 1, Appl
8	238	9.7	4665	5 US-08-564-313-1	Sequence 1, Appl
9	238	9.7	4665	5 US-08-564-313-1	Sequence 1, Appl
10	232.8	9.5	276	1 US-08-127-954-134	Sequence 134, App
11	232.8	9.5	276	1 US-08-127-954-140	Sequence 40, App
12	229.6	9.4	276	1 US-08-127-954-111	Sequence 111, App
13	228	9.3	276	1 US-08-127-954-109	Sequence 109, App
14	226.4	9.3	276	1 US-08-127-954-110	Sequence 110, App
15	224.8	9.2	276	1 US-08-127-954-101	Sequence 101, App
16	223.2	9.1	276	1 US-08-127-954-96	Sequence 96, App
17	223.2	9.1	276	1 US-08-127-954-99	Sequence 99, App
18	223.2	9.1	276	1 US-08-127-954-108	Sequence 108, App
19	223.2	9.1	276	1 US-08-127-954-116	Sequence 116, App
20	223.2	9.1	276	1 US-08-127-954-117	Sequence 117, App
21	223.2	9.1	276	1 US-08-127-954-118	Sequence 118, App
22	223.2	9.1	276	1 US-08-127-954-131	Sequence 131, App
23	221.6	9.1	276	1 US-08-127-954-95	Sequence 95, App
24	221.6	9.1	276	1 US-08-127-954-100	Sequence 100, App
25	221.6	9.1	276	1 US-08-127-954-102	Sequence 102, App
26	221.6	9.1	276	1 US-08-127-954-103	Sequence 103, App
27	221.6	9.1	276	1 US-08-127-954-105	Sequence 105, App

28	221.6	9.1	276	1 US-08-127-954-119	Sequence 119, App
29	221.6	9.1	276	1 US-08-127-954-120	Sequence 120, App
30	221.6	9.1	276	1 US-08-127-954-121	Sequence 121, App
31	221.6	9.1	276	1 US-08-127-954-123	Sequence 123, App
32	221.6	9.1	276	1 US-08-127-954-132	Sequence 132, App
33	221.6	9.1	276	1 US-08-127-954-133	Sequence 133, App
34	220	9.0	276	1 US-08-127-954-97	Sequence 97, App
35	220	9.0	276	1 US-08-127-954-98	Sequence 98, App
36	220	9.0	276	1 US-08-127-954-104	Sequence 104, App
37	220	9.0	276	1 US-08-127-954-115	Sequence 115, App
38	220	9.0	276	1 US-08-127-954-129	Sequence 129, App
39	220	9.0	276	1 US-08-127-954-130	Sequence 130, App
40	218.4	8.9	276	1 US-08-127-954-113	Sequence 113, App
41	218.4	8.9	276	1 US-08-127-954-114	Sequence 114, App
42	218.4	8.9	276	1 US-08-127-954-122	Sequence 122, App
43	218.4	8.9	276	1 US-08-127-954-126	Sequence 126, App
44	218.4	8.9	276	1 US-08-127-954-127	Sequence 127, App
45	218.4	8.9	276	1 US-08-127-954-127	Sequence 127, App

## ALIGNMENTS

```

RESULT 1
US-08-522-942-1
: Sequence 1, Application US/08522942
: Patent No. 5753442
: GENERAL INFORMATION:
: APPLICANT: Tyan, Dolly B.
: TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC
: TITLE OF INVENTION: PRESTIPROPOSITION FOR SEMONAGATIVE SPONDYLARTHROPHATHIES AND
: NUMBER OF INVENTIONS: 8
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Pretty, Schroeder, Brueggemann & Clark
: STREET: 4365 Executive Drive, Suite 1500
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92121
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/522,942
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ramos, Robert T.
: REGISTRATION NUMBER: 37,915
: REFERENCE/DOCKET NUMBER: P07 33624
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-546-1995
: TELEFAX: 619-546-9392
: INFORMATION FOR SEQ. ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6553 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: DNA (genomic)
: US-08-522-942-1

```

Query Match 57.9% Score 1415; DB 1; Length 6553;  
Best Local Similarity 79.1%; Pred. No. 0;  
Matches 1963; Conservative 0; Mismatches 380; Indels 140; Gaps 18;

QY 5 CCCGAGTCTCCGGGCTCGGATCC-ACCCGAGGCGCGGACCCGCCAGACCTTAC 63  
|||||  
Db 1215 CCCGAGTCTCCGGGCTCGGATCCGCCCGGAGGCGGACCCGCCAGACCTTAC 1274



Db 3340 GTGTCTCTCAACAGCTTGAAGAAGTGAGATCTTGGGCTCTAGAGTGGGCTGGCCAGG 3399  
 Oy 2242 TGTGGGTTTGTGAGGGGACAGGACATGCTGTCTGTAGAGTTTCTTGCATCTCAAT 2301  
 Db 3400 TCTGGGGGTGGGTGGGACCTGAGGAAAGCCCTGATAGGATTTCTTGCATCTGGAT 3459  
 Oy 2302 GTATGAGCATGTGATGGCTGTAAAGTGTGACCCCTGACGTGACATGATGATTT 2361  
 Db 3460 GTTTCGGCTGTGTGGTGGCTGTGTAGACGTGATCATCTTACCATGACACCAATTT 3519  
 Oy 2362 GTTATGATAT--TTTCTGTAGTGAACAGCTGCCCTGTGGGACGTGAGTGGCAA 2419  
 Db 3520 GTTCATGATGTTGTTTCTGTAGCCTGAGACAGCTGTCTGTGAGGAGCTGATGAG 3579  
 Oy 2420 GATTGTTCAAGCCTTCCCTTTG 2442  
 Db 3580 GATTCTTCAAGCCTTCCCTTTG 3602

## RESULT 2

US-08-577-081A-3  
 ; Sequence 3, Application US/08577081A  
 ; Patent No. 6030775

## GENERAL INFORMATION:

APPLICANT: Yang, Soo Young  
 APPLICANT: Cereb, Nezh  
 TITLE OF INVENTION: Methods and Reagents for Typing HLA  
 NUMBER OF SEQUENCES: 84  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Opedahl & Larson  
 STREET: 1992 Commerce Street Suite 309  
 CITY: Yorktown  
 STATE: NY  
 COUNTRY: US  
 ZIP: 10598  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: Word Perfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/577,081A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Larson, Marina T.  
 REGISTRATION NUMBER: 32,038  
 REFERENCE/DOCKET NUMBER: MSK-P-001-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (914) 245-3252  
 TELEFAX: (914) 962-4330  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 600  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 HYPOTHEICAL: no  
 ANTI-SENSE: no  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 ORGANISM: human  
 FEATURE:  
 OTHER INFORMATION: consensus sequence of Intron 3 of the  
 OTHER INFORMATION: HLA-A gene  
 US-08-577-081A-3

Query Match 17.5%: Score 426.8; DB 3; Length 600;  
 Best Local Similarity 81.6%: Pred. No. 3.7e-110;  
 Matches 493; Conservative 37; Mismatches 65; Indels 9; Gaps 4;  
 Oy 438 GTACAGGGGCGAGTGGGGGCGCTCCGTGATCTCTGTAGACCTCTGAGCTGAGCTGAGCA 497  
 Db 1 GTACAGGGGCGAGTGGGGGCGCTCCGTGATCTCTGTAGACCTCTGAGCTGAGCTGAGCA 60  
 Oy 498 CAAG 557  
 Db 61 CAAG 120  
 Oy 558 AG 617  
 Db 121 AG 180  
 Oy 618 GCTCTGTGAG 677  
 Db 181 GCTCTGTGAG 239  
 Oy 678 GAAG 732  
 Db 240 GAAG 299  
 Oy 733 TCCCTGAG 792  
 Db 300 TCCCTGAG 359  
 Oy 793 CTCTGAG 852  
 Db 360 CTCTGAG 418  
 Oy 853 GAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 912  
 Db 419 GAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 478  
 Oy 913 GGGTGTGTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 972  
 Db 479 GGGTGTGTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 538  
 Oy 973 AGGTGCTGCTGAG 1032  
 Db 539 --RTGCTGAG 596  
 Oy 1033 TCAG 1036  
 Db 597 WCAG 600

## RESULT 3

US-08-577-081A-9  
 ; Sequence 9, Application US/08577081A  
 ; Patent No. 6030775

## GENERAL INFORMATION:

APPLICANT: Yang, Soo Young  
 APPLICANT: Cereb, Nezh  
 TITLE OF INVENTION: Methods and Reagents for Typing HLA  
 NUMBER OF SEQUENCES: 84  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Opedahl & Larson  
 STREET: 1992 Commerce Street Suite 309  
 CITY: Yorktown  
 STATE: NY  
 COUNTRY: US  
 ZIP: 10598  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: Word Perfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/577,081A

Page 4

```

01 1025 TCCTCCCTTCAG 1036
02      ||||| |||
03 Db      576 TCCTCCCGTCAG 587

04 RESULT 4
05 US-08-577-081A-6
06 ; Sequence 6, Application US/08577081A
07 ; Patent No. 6030775
08 ;
09 ; GENERAL INFORMATION:
10 ;
11 ; APPLICANT: Yang, Soo Young
12 ;
13 ; APPLICANT: Cered, Nezh
14 ;
15 ; TITLE OF INVENTION: Methods and Reagents for Typing HLA
16 ;
17 ; TITLE OF INVENTION: Class I Genes
18 ;
19 ; NUMBER OF SEQUENCES: 84
20 ;
21 ; CORRESPONDENCE ADDRES:
22 ;
23 ; ADDRESSEE: Opedahl & Larson
24 ;
25 ; STREET: 1992 Commerce Street Suite 309
26 ;
27 ; CITY: Yorktown
28 ;
29 ; STATE: NY
30 ;
31 ; COUNTRY: US
32 ;
33 ; ZIP: 10598
34 ;
35 ; COMPUTER READABLE FORM:
36 ;
37 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
38 ;
39 ; COMPUTER: IBM compatible
40 ;
41 ; OPERATING SYSTEM: MS DOS
42 ;
43 ; SOFTWARE: Word Perfect
44 ;
45 ; CURRENT APPLICATION DATA:

```

```

FLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: MSK-P-001-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 575
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
OTHER INFORMATION: consensus sequence of Intron 3 of the
? ? ? ? ?
OTHER INFORMATION: HLA-B gene
US-08-577-081A-6

Query Match 13.8%; Score 335.8; DB 3; Length 575;
Best Local Similarity 76.4%; Pred. No. 1,3e-84;
Matches 439; Conservative 28; Mismatches 86; Indels 28; Gaps

QY 438 GTACGAGGGGCGAGTGGGGGCGCTCCTCGATCCTCCTGTAGACCTTCACGCTGAGCCATGACA 497
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GTACCGAGGGGCGAGTGGGGGCGCTCCTCGATCCTCCTGTAGACCTTCACGCTGAGCCATGACA 60

498 CAGGAGGAGGAGCAAAATGGGACACACATGAAATATGCGCCCTCGCTGCGTCTCGAGGG 557
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 CGAGAGAGAGAGAGAAATGGGATCAGCCGCTGAGATGTGCGCTCCTCGTGAATGAGAAATG 1207
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

558 AGAGGATCCTCTCGGTGGTTTCAGATCCTGTACCGAGAGATGATTCGTGAGGGCCCGTCT 617

```



```

Db 121 GCATGATTTTCTGAGTTTC-----TCTGAGGGGCCCCCT 158
Qy 618 GCTCTGGGCAATTAGGATAGTCTGTGAGGAGTGGAGGGAAGACATCCCG 677
Db 159 TCTCTTAGACATTAAGATACGCTCTGTAGGAAATGAGGGAAGACATCCCTA 218
Qy 678 GAAGACTATCAGGGGTTCCCTTTGACCCC-ACAGACCTT-6GACAGGACTTTTC 735
Db 219 GATATGATCAGGGGTCCTTTGACCCCTGACAGCTTGGAAACCTGACTTTCT 278
Qy 736 CCTGAGGCTTCTCTGCTGCTCAGCTCATGATGTGTGGGGTGTGACCTCAGCTCC 795
Db 279 TCTCAGGCTTGTCTGTGCTCAGCTCATGATGTGTGGGGTGTGACCTCAGCTCC 855
Qy 796 TGAGTCCCTTGGCTTCAGTCTGAGTCTGAGAACGGAGGTCCTCCCGCTCAGAGAC 855
Db 339 TGAGTCACTTACCTCCAGCTCAGATCRGAGCAGAGACTCTCTG-TTCCCGCTCAGAGAC 855
Qy 856 TGAGTCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTG 915
Db 398 TCGAATCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTG 915
Qy 916 TCTGTGCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTG 975
Db 458 TCTGTGCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTG 975
Qy 976 TCTGTGCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTG 1035
Db 515 TGTGCTTCCAGGATATGAGATATATCCAGGTGCTGCTGCTGCTGCTGCTGCTG 574
Qy 1036 G 1036
Db 575 G 575

RESULT 5
US-08-577-081A-52
; Sequence 52, Application US/08577081A
; Patent No. 6030775
; GENERAL INFORMATION:
; APPLICANT: Yang, Soo Young
; APPLICANT: Cereb, Nezh
; TITLE OF INVENTION: Methods and Reagents for Typing HLA
; TITLE OF INVENTION: Class I Genes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: 1992 Commerce Street Suite 309
; CITY: Yorktown
; STATE: NY
; COUNTRY: US
; ZIP: 10598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,081A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: MSK-P-001-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:

```

```

; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: consensus sequence of intron 3 of the
; OTHER INFORMATION: HLA-F gene
US-08-577-081A-52

Query Match 10.2%; Score 249.2; DB 3; Length 544;
Best Local Similarity 76.5%; Pred. No. 2.5e-60;
Matches 442; Conservative 0; Mismatches 83; Indels 53; Gaps 9;

Qy 453 GGGCGCTCCCTGATCTCTGTGACCTCTGACCTGAGTCTGAGGAGGAGGAGAA 512
Db 15 GGGCGCTCCCTGATCTCTGTGACCTCTGAGTCTGAGGAGGAGGAGGAGAA 74
Qy 513 ATGGGACCAACATGATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
Db 75 AGTGGGACCAACATGATATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 134
Qy 573 G-GTTTCAGATCTCTGACAGAGATATTCGAGGAGGAGGAGGAGGAGGAGGAG 631
Db 135 GCTTTTCAGATCTCTGACAGAGATATTCGAGGAGGAGGAGGAGGAGGAGGAG 194
Qy 632 TTAAGGATGATGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
Db 195 TTAAGGATGATGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 225
Qy 692 GGTTCCTTTGACCCAGCAGAGACCTTGGACAGGAGGAGGAGGAGGAGGAGGAG 751
Db 226 GGTTCCTTTGACCCAGCAGAGACCTTGGACAGGAGGAGGAGGAGGAGGAGGAG 278
Qy 752 CTGCTTCACTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 811
Db 279 CTGCTTCACTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 328
Qy 812 CACTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
Db 329 CACTTACTGAGG--CCAGAGATCCCTGCT--CCGCTCAGAGACTCGAAGCTTCCAGAG 384
Qy 872 ATAGGATATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 931
Db 385 ATAGGATATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 444
Qy 932 CCACCCAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 991
Db 445 CCACCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
Qy 992 CAGGAGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1029
Db 503 CATGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

RESULT 6
US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marguet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2

```

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson and Bear  
 STREET: 620 Newport Center Drive 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/564,313

FILING DATE: 01-DEC-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/074,344

FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Israelson, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: VICAL.033CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4059 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: circular

HYPOTHEetical: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

IMMEDIATE SOURCE:

CLONE: HLA-B7

US-08-564-313-2

Query Match 9.7%; Score 238; DB 2; Length 4059;

Best Local Similarity 91.0%; Pred. No. 9.3e-57;

Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1034 CAGACCCCCCAAGACACAGTACACCCCTGCTTTGACTATGAGGCCACCTGA 1093  
 DB 2267 CTGACCCCAAGACACAGTACACCCCTGCTTTGACTATGAGGCCACCTGA 2208  
 QY 1094 GGTGCTGGGCGCTGCTTACCTGCGGAGATCATCTGACCTGGGAGGCGATGGG 1153  
 DB 2207 GGTGCTGGGCGCTGCTTACCTGCGGAGATCATCTGACCTGGGAGGCGATGGG 2148  
 QY 1154 AGGACCAACCCAGGACCTGAGCTGTGAGAGCCAGGCGCTGAGGAGTGAACCTTC 1213  
 DB 2147 AGGACCAACCCAGGACCTGAGCTGTGAGAGCCAGGCGCTGAGGAGTGAACCTTC 2088  
 QY 1214 AGAAGTGGGACGCTGTGTGTGCTTCTGAGAGAGCAGAGATACAGTCCATGTGC 1273  
 DB 2087 AGAAGTGGGACGCTGTGTGTGCTTCTGAGAGAGCAGAGATACAGTCCATGTGC 2028  
 QY 1274 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATGG 1311  
 DB 2027 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATGG 1990

## RESULT 7

PCT-US94-06069-2/c

Sequence 2, Application PC/TUS9406069

GENERAL INFORMATION:

APPLICANT: Vical Incorporated

APPLICANT: Regents of the University of Michigan

APPLICANT: Nabel, Elizabeth

## APPLICANT: Nabel, Gary

ADDRESSEE: Lew, Denise  
 STREET: 620 Newport Center Drive 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06069

FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Israelson, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: VICAL.033VPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4059 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: circular

HYPOTHEtical: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

STRAIN: HLA-B7

PCT-US94-06069-2

Query Match 9.7%; Score 238; DB 5; Length 4059;

Best Local Similarity 91.0%; Pred. No. 9.3e-57;

Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1034 CAGACCCCAAGACACAGTACACCCCTGCTTTGACTATGAGGCCACCTGA 1093  
 DB 2267 CTGACCCCAAGACACAGTACACCCCTGCTTTGACTATGAGGCCACCTGA 2208  
 QY 1094 GGTGCTGGGCGCTGCTTACCTGCGGAGATCATCTGACCTGGGAGGCGATGGG 1153  
 DB 2207 GGTGCTGGGCGCTGCTTACCTGCGGAGATCATCTGACCTGGGAGGCGATGGG 2148  
 QY 1154 AGGACCAACCCAGGACCTGAGCTGTGAGAGCCAGGCGCTGAGGAGTGAACCTTC 1213  
 DB 2147 AGGACCAACCCAGGACCTGAGCTGTGAGAGCCAGGCGCTGAGGAGTGAACCTTC 2088  
 QY 1214 AGAAGTGGGACGCTGTGTGTGCTTCTGAGAGAGCAGAGATACAGTCCATGTGC 1273  
 DB 2087 AGAAGTGGGACGCTGTGTGTGCTTCTGAGAGAGCAGAGATACAGTCCATGTGC 2028  
 QY 1274 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATGG 1311  
 DB 2027 AGCATGAGGGGCTGCGGAGCCCTCATGCTGAGATGG 1990

## RESULT 8

US-08-564-313-1

```
Sequence 1, Application US/08564313
Patent No. 5910488
GENERAL INFORMATION:
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marguet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
IMMEDIATE SOURCE:
CLONE: HLA-B7 and Beta-2
US-08-564-313-1
Query Match 9.7%; Score 238; DB 2; Length 4965;
Best Local Similarity 91.0%; Pred. No. 1e-56;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

```
RESULT 9
PCT-US94-06069-1
Sequence 1, Application PC/TUS9406069
GENERAL INFORMATION:
APPLICANT: Vical Incorporated
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marguet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1
Query Match 9.7%; Score 238; DB 5; Length 4965;
Best Local Similarity 91.0%; Pred. No. 1e-56;
Matches 253; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
```

Db 1331 AGAAGTGGGCAAGCTGTGTGTCCTTCTGAGAGAGAGATACATCCATGTAC 1390

QY 1274 AGCATGAGGGGCTGCCGAGACCCCTCATGCTGAGATGG 1311

Db 1391 AGCATGAGGGGCTGCCGAGAGCCCTCATGCTGAGATGG 1428

# RESULT 10

US-08-127-954-134

; Sequence 134, Application US/08127954

; Patent No. 5451512

; GENERAL INFORMATION:

; APPLICANT: Apple, Raymond J.

; APPLICANT: Bugawan, Teodorica L.

; APPLICANT: Erlich, Henry A.

; TITLE OF INVENTION: Methods and Reagents for HLA Class I A

; NUMBER OF SEQUENCES: 173

; CORRESPONDENCE ADDRESS:

; ADDRESS: Hoffmann-La Roche Inc.

; STREET: 340 Kingsland Street

; CITY: Nutley

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07110-1199

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/127,954

; FILING DATE:

; CLASSIFICATION: 436

; ATTORNEY/AGENT INFORMATION:

; NAME: Petty, Douglas A.

; REGISTRATION NUMBER: 35,321

; REFERENCE/DOCKET NUMBER: 8873

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 814-2974

; TELEFAX: (510) 814-2974

; INFORMATION FOR SEQ ID NO: 134:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 276 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

Query Match 9.5%; Score 232.8; DB 1; Length 276;

Best Local Similarity 90.2%; Pred. No. 76-56;

Matches 249; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 162 GTTCTCACACCTTCAGTGTGATGCTGCGACCTGAGGATCCGACGAGCCTCTCC 221

Db 1 GGTCTCACACCTTCAGTGTGATGCTGCGACCTGAGGATCCGACGAGCCTCTCC 60

QY 222 GGGGATATGACAGTATGCTACGATGCGCAAGGATTACCTCGCCCGCAAGAGAGACCTGC 281

Db 61 GGGGATATGACAGTATGCTACGATGCGCAAGGATTACCTCGCCCGCAAGAGAGACCTGC 120

QY 282 GCTCTGACCGCAGCGACACTGCGCTCATATCTCCAAAGCGCAAGTGTGAGCGGCCA 341

Db 121 GCTCTGACCGCAGCGACACTGCGCTCATATCTCCAAAGCGCAAGTGTGAGCGGCCA 180

QY 342 ATGTGGTGAACAAAGAGAGAGCTTACCTGAGAGGAGAGCTGAGAGAGAGAGAGAGAT 401

Db 181 GTGTGGGAGACAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240

QY 402 ACCTGAT 437

Db 241 ACCTGAT 276

# RESULT 11

US-08-577-081A-40

; Sequence 40, Application US/08577081A

; Patent No. 6030775

; GENERAL INFORMATION:

; APPLICANT: Yang, Soo Young

; APPLICANT: Cereb, Nezh

; TITLE OF INVENTION: Methods and Reagents for Typing HLA

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESS: Oppedahl & Larson

; STREET: 1992 Commerce Street Suite 309

; CITY: Yorktown

; STATE: NY

; COUNTRY: US

; ZIP: 10598

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/577,081A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Larson, Marina T.

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: MSK-P-001-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 276

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; HYPOTHETICAL: no

; ANTI-SENSE: no

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: human

; FEATURE:

; OTHER INFORMATION: consensus sequence of exon 3 of the

; OTHER INFORMATION: nonclassical HLA genes

US-08-577-081A-40

Query Match 9.5%; Score 232.8; DB 3; Length 276;

Best Local Similarity 90.2%; Pred. No. 76-56;

Matches 249; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 162 GTTCTCACACCTTCAGTGTGATGCTGCGACCTGAGGATCCGACGAGCCTCTCC 221

Db 1 GGTCTCACACCTTCAGTGTGATGCTGCGACCTGAGGATCCGACGAGCCTCTCC 60

QY 222 GGGGATATGACAGTATGCTACGATGCGCAAGGATTACCTCGCCCGCAAGAGAGACCTGC 281

Db 61 GGGGATATGACAGTATGCTACGATGCGCAAGGATTACCTCGCCCGCAAGAGAGACCTGC 120

QY 282 GCTCTGACCGCAGCGACACTGCGCTCATATCTCCAAAGCGCAAGTGTGAGCGGCCA 341

Db 121 GCTCTGACCGCAGCGACACTGCGCTCATATCTCCAAAGCGCAAGTGTGAGCGGCCA 180

QY 342 ATGTGGTGAACAAAGAT 401



```

: Sequence 110, Application us/08127954
: Patent No. 5451512
: GENERAL INFORMATION:
: APPLICANT: Apple, Raymond J.
: APPLICANT: Bugawan, Teodorica L.
: APPLICANT: Erlich, Henry A.
: TITLE OF INVENTION: Methods and Reagents for HLA Class I A
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: U.S.A.
: ZIP: 07110-1199
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127,954
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Petry, Douglas A.
: REGISTRATION NUMBER: 35,321
: REFERENCE/DOCKET NUMBER: 8873
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 814-2974
: TELEFAX: (510) 814-2977
: INFORMATION FOR SEQ ID NO: 110:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 276 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-127-954-110

Query Match
Best Local Similarity 9.3%; Score 226.4; DB 1; Length 276;
Matches 245; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 162 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCCTCTCC 221
DB 1 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCCTCTCC 60
QY 222 GCGGGTATGACAGTATGCTCTAGCATGSCAAGATTACTCGCCCTGAAGAGACCTGC 281
DB 61 GCGGGTATGACAGTATGCTCTAGCATGSCAAGATTACTCGCCCTGAAGAGACCTGC 120
QY 282 GCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 341
DB 121 GCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
QY 342 ATGTGGCTTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
DB 181 ATGTGGCTTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240
QY 402 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
DB 241 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276

```

## RESULT 15

US-08-127-954-101

Sequence 101, Application US/08127954

Patent No. 5451512

GENERAL INFORMATION:

APPLICANT: Apple, Raymond J.

APPLICANT: Bugawan, Teodorica L.

APPLICANT:

```

: APPLICANT: Erlich, Henry A.
: TITLE OF INVENTION: Methods and Reagents for HLA Class I A
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: U.S.A.
: ZIP: 07110-1199
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127,954
: FILING DATE:
: CLASSIFICATION: 436
: ATTORNEY/AGENT INFORMATION:
: NAME: Petry, Douglas A.
: REGISTRATION NUMBER: 35,321
: REFERENCE/DOCKET NUMBER: 8873
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (510) 814-2974
: TELEFAX: (510) 814-2977
: INFORMATION FOR SEQ ID NO: 101:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 276 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-127-954-101

Query Match
Best Local Similarity 9.2%; Score 224.8; DB 1; Length 276;
Matches 244; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 162 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCCTCTCC 221
DB 1 GTTCTACACCCCTCCAGTATGATGCTGCGACCTGGGCTCCGACGAGCCCTCTCC 60
QY 222 GCGGGTATGACAGTATGCTCTAGCATGSCAAGATTACTCGCCCTGAAGAGAGACTGC 281
DB 61 GCGGGTATGACAGTATGCTCTAGCATGSCAAGATTACTCGCCCTGAAGAGAGACTGC 120
QY 282 GCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 341
DB 121 GCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
QY 342 ATGTGGCTTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
DB 181 ATGTGGCTTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240
QY 402 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
DB 241 ACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276

```

Search completed: January 31, 2003, 00:52:52  
 Job time : 122 secs